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OM protein - protein search, using sw model

                    GenCore version 4.5
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Run on:             September 28, 2000, 17:01:17 ; Search time 47.46 seconds
                                                   (without alignments)
                                                   220.092 Million cell updates/sec

Title:              US-09-142-613-1
Perfect score:      2295
Sequence:           1 MAEPRQEFEVMEDHAGQDTY..........SPQLATLADEVSASLAKQGL 441

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters:      188963

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:    Minimum Match 0%
                    Maximum Match 100%
                    Listing first 45 summaries

Database :          A_Geneseq_36:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2295	100.0	441	1	W34856	Human tau protein.
2	2262	98.6	441	1	R58810	Human tau protein.
3	2223	96.9	441	1	W05282	Human tau protein.
4	1983	86.4	390	1	W05283	Truncated human ta
5	1719.5	74.9	352	1	P91294	Paired helical fil
6	1719.5	74.9	352	1	R32708	Human tau-protein.
7	739	32.2	1717	1	W23331	Neuroblastoma indi
8	733	31.9	140	1	W05285	Human tau protein
9	713.5	31.1	1831	1	W23329	Microtubule-associ
10	593	25.8	112	1	R76937	PHF-tau (143-254)
11	563	24.5	106	1	R92516	Microtubule-associ
12	551	24.0	140	1	W05286	Fragment of microt
13	364	21.8	95	1	W05284	Human tau protein
14	364	15.9	67	1	R59837	Sequence of human
15	270	11.8	55	1	W34876	Human tau protein
16	217	9.5	42	1	R98431	Tau40 epitope (res
17	185	8.1	34	1	R61330	Peptide phosphoryl
18	185	8.1	34	1	W34875	Human tau protein
19	172.5	7.5	455	1	R46606	Malarial PfEMP3 ep
20	172.5	7.5	1663	1	R46608	Plasmodium falcipa
21	159.5	6.9	1404	1	R26049	MSF precursor. New
22	157	6.8	984	1	R85782	Group B Streptococ
23	157	6.8	1093	1	W40540	Mutant C-beta prot
24	157	6.8	1099	1	W40538	Mutant C-beta prot
25	157	6.8	1128	1	W40539	Mutant C-beta prot
26	157	6.8	1164	1	R85781	Group B streptococ
27	157	6.8	1164	1	W40537	Group B streptococ
28	157	6.8	1164	1	W40541	Mutant C-beta prot
29	154	6.7	1664	1	W43106	C. thermocellum Ol
30	153	6.7	783	1	W70586	Human SLAP-130. Nu
31	150.5	6.6	976	1	W02289	Mouse neuron restr
32	150	6.5	649	1	W67883	Human secreted pro
33	150	6.5	1187	1	R66451	AF-4 protein (enco
34	150	6.5	1210	1	R66450	AF-4 protein (enco
35	148	6.4	818	1	W72035	HSV-2 strain SB5 C
36	148	6.4	1896	1	W72095	HSV-2 strain SB5 C
37	148	6.4	3119	1	W72204	HSV-2 strain SB5 C
38	147.5	6.4	1060	1	Y01540	Trypanosoma cruzi
39	147	6.4	1196	1	Y01916	Type III procollag
40	146	6.4	1780	1	R28916	Human gravin polyp
41	145.5	6.3	1313	1	W53863	Spinocerebellar at
42	145	6.3	914	1	W60213	Spinocerebellar at
43	145	6.3	1312	1	W24800	Spinocerebellar at
44	145	6.3	1312	1	W33807	Human ataxin-2. Nu
45	142.5	6.2	793	1	W73307	HL60 cell line pro
	142.5	6.2	452	1	R80041	Human megakaryocyt

ALIGNMENTS

RESULT 1

```
ID   W34856 standard; protein; 441 AA.
AC   W34856;
DT   27-MAR-1998  (first entry)
DE   Human tau protein.
KW   detection; phosphorylated tau protein; paired helical filament;
KW   Antibody; Phosphorylated tau protein; Alzheimer's disease; human.
OS   Homo sapiens.
PN   WO9734145-A1.
PD   18-SEP-1997.
PF   13-MAR-1997; J00804.
PR   13-MAR-1996; JP-056090.
PA   (MITU ) MITSUBISHI CHEM CORP.
PI   Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
DR   WPI; 97-470978/43.
PT   Phosphorylated tau protein; used for detecting Alzheimer's disease
PT   Antibody prepared using a partial peptide containing part of
PT   phosphorylated tau protein - used for detecting Alzheimer's disease
CC   Claim 2; Pages 25-27; 48pp; Japanese.
CC   Claim 1: Pages 25-27; 48pp; Japanese.
CC   An antibody, prepared using a partial peptide containing the
CC   phosphorylated residue of the phosphorylated tau protein, e.g. the
CC   present sequence, in a paired helical filament, can be used to
CC   detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC   protein in brain extracts or tissue fragments.
SQ   Sequence  441 AA;

Query Match        100.0%;  Score 2295;  DB 1;  Length 441;
Best Local Similarity   100.0%;
Matches  441;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMHQDEGDTDAGLKESPLQTPTEDGSEEPG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMHQDEGDTDAGLKESPLQTPTEDGSEEPG 60

Qy   61 SETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 SETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAG 120

Qy  121 HVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPK 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 HVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPK 180

Qy  181 TPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAK 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAK 240

Qy  241 SRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHV 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 SRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHV 300

Qy  301 PGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNI 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 PGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNI 360

Qy  361 THVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMV 420
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Db  361 THVPGGGNKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMV 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  421 DSPQLATLADEVSASLAKQGL 441
         |||||||||||||||||||||
Db  421 DSPQLATLADEVSASLAKQGL 441
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RESULT 2
R58810
ID   R58810 standard; protein; 441 AA.
AC   R58810;
DT   27-MAR-1995 (first entry)
DE   Human tau protein.
KW   Tau; cerebrospinal fluid; immunoassay; antibody; detection;
KW   diagnosis; central nervous system; CNS; cytopathies; cytopathy;
KW   Alzheimer's disease.
OS   Homo sapiens.
PN   WO9418560-A.
PD   18-AUG-1994;
PF   10-FEB-1994;
PR   12-FEB-1993; JP-046133.
PA   (TEIJ) TEIJIN LTD.
PI   Eguchi H, Hosoda K, Kobayashi S, Kubota T, Mori H;
PI   Nakamoto T;
DR   WPI; 94-279910/34.
PT   Sandwich immunoassay of tau protein in cerebrospinal fluid - for
PT   diagnosis of Alzheimer's disease and other CNS cytopathies
PS   Claim 1; Page 16-18; 36pp; Japanese.
CC   Detection of the human tau protein (or fragments of it) in samples
CC   of cerebrospinal fluid enables the diagnosis of central nervous
CC   system cytopathies such as Alzheimer's disease. Detection is
CC   performed using labelled antibodies which recognise sites within the
CC   region defined by the amino acid residues 251-441. The antibodies
CC   are preferably polyclonal.
SQ   Sequence 441 AA;

Query Match   98.6%; Score 2262; DB 1; Length 441;
Best Local Similarity 99.8%; Pred. No. 2.7e-150;
Matches 439; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

Qy   1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE 58
         ||||||||||||||||| |||||||||||||||| ||||||||||||||||||||||||
Db   1 MAEPRQEFEVMEDHAG--TYGLGDKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEE 58

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118

Qy 119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178

Qy 179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPKSPSS 238
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPKSPSS 238

Qy 239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298

Qy 299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358

Qy 359 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 359 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418

Qy 419 MVDSPQLATLADEVSASLAKQGL 441
         |||||||||||||||||||||||
Db 419 MVDSPQLATLADEVSASLAKQGL 441
```

RESULT 3
W05282
ID   W05282 standard; Protein; 441 AA.
AC   W05282;
DT   20-DEC-1996 (first entry)
DE   Human tau protein.
KW   Tau protein; inhibition; modulation; prophylaxis; treatment;
KW   Alzheimer's disease; motor neurone disease; Lewy body disease;
KW   progressive supranuclear palsy; Pick's disease.
OS   Homo sapiens.
PN   WO9630766-A1.
PD   03-OCT-1996.
PF   25-MAR-1996; E01307.
PR   27-MAR-1995; GB-006197.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PI   Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
DR   WPI; 96-455570/45.
DR   N-PSDB; T39591.
PT   Assay for inhibitors of tau-tau interaction - used for identifying
PT   cpds., partic. phenothiazine cpds., for treating pathological
PT   tau-tau or neuro:filament aggregation
PS   Example 2; Page 53-54; 97pp; English.
CC   Detecting an agent which modulates or inhibits tau-tau protein
CC   association comprises contacting two tau proteins, distinct from
CC   each other yet capable of binding to the other and where one of the
CC   tau proteins is labelled, in the presence of the agent suspected of
CC   being capable of modulating or inhibiting tau-tau interaction.
CC   Agents identified as being modulators or inhibitors of tau-tau
CC   interaction may be used for the prophylaxis and treatment of
CC   Alzheimer's disease, motor neurone disease, Lewy body disease,
CC   Pick's disease or progressive supranuclear palsy.
SQ   Sequence 441 AA;

Query Match       96.9%;  Score 2223;  DB 1;  Length 441;
Best Local Similarity  98.0%;  Pred. No. 1.4e-147;
Matches  434;  Conservative  0;  Mismatches  5;  Indels  4;  Gaps  2;

Qy    1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE 58
         ||||||||||||||||| ||||||||||||||||  ||||||||||||||||||||||||
Db    1 MAEPRQEFEVMEDHAG--TYGLGDKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEE 58

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118

Qy  119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178

Qy  179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPKSLSS 238
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPKSLSS 238

Qy  239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298

Qy  299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  299 QVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358

Qy  359 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418
         ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  359 NITHVPGGGNKKIETHKLTVRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418

Qy  419 MVDSPQLATLADEVSASLAKQGL 441
         |||||||||||||  ||||||||
Db  419 MVDSPQLATLADEGSASLAKQGL 441
```

RESULT 4

W05283

ID   W05283 standard; protein; 390 AA.
AC   W05283;
DT   20-DEC-1996 (first entry)
DE   Truncated human tau protein.
KW   Tau protein; inhibition; modulation; prophylaxis; treatment;
KW   Alzheimer's disease; motor neurone disease; Lewy body disease;
KW   progressive supranuclear palsy; Pick's disease.
OS   Homo sapiens.
PN   WO9630766-A1.
PD   03-OCT-1996.
PF   25-MAR-1996;
PR   27-MAR-1995; GB-006197.
PA   (HOFF) HOFFMANN LA ROCHE & CO AG F.
PI   Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
DR   WPI; 96-455570/45.
DR   E01307.
PT   Assay for inhibitors of tau-tau interaction - used for identifying
PT   cpds., partic. phenothiazine cpds., for treating pathological
PT   tau-tau or neuro:filament aggregation
PS   Claim 11; 97pp; English.
CC   Detecting an agent which modulates or inhibits tau-tau protein
CC   association comprises contacting two tau proteins, distinct from
CC   each other yet capable of binding to the other and where one of the
CC   tau proteins is labelled, in the presence of the agent suspected of
CC   being capable of modulating or inhibiting tau-tau interaction.
CC   Agents identified as being modulators or inhibitors of tau-tau
CC   interaction may be used for the prophylaxis and treatment of
CC   Alzheimer's disease, motor neurone disease, Lewy body disease,
CC   Pick's disease or progressive supranuclear palsy. This sequence of
CC   the human tau protein is truncated at amino acid residue 390. The
CC   full length protein is given in W05282.
SQ   Sequence 390 AA;

Query Match   86.4%; Score 1983; DB 1; Length 390;
Best Local Similarity   98.0%;
Matches 384; Conservative   0; Mismatches   4; Indels   4; Gaps   2;

Qy   1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE 58
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   1 MAEPRQEFEVMEDHAG--TYGLGDRKDQGGYTMHQDEGDTDAGLKESPLQTPTEDGSEE 58

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118

Qy   119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178

Qy   179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 238
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 238

Qy   239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298

Qy   299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358

Qy   359 NITHVPGGGNKKIETHKLTFRENAKAKTDHGA 390
          ||||||||||||||||||||||||||||||||
Db   359 NITHVPGGGNKKIETHKLTFRENAKAKTDHGA 390

RESULT 5

P91294
ID   P91294 standard; protein; 352 AA.
AC   P91294;
DT   10-MAR-1993 (revised)

DT   18-DEC-1989 (first entry)
DE   Paired helical filament (PHF) core protein.
KW   Paired helical filament (PHF) core protein; Alzheimer's disease;
KW   neurofibrillary tangles.
OS   Homo sapiens.
PN   WO8903993-A.
PD   05-MAY-1989.
PF   19-OCT-1988; G00867.
PF   19-OCT-1987; GB-024412.
PA   (MEDI) Medical Research Council.
PI   Wischik CM, Milstein C, Klug A;
DR   WPI; 89-150854/20.
PT   Paired helical filament core protein - used for providing reagents
PT   sensitive to neurofibrillary tangles used for diagnosing Alzheimer's
PT   disease.
PS   Disclosure; fig 1; 29pp; English.
CC   Paired helical filament core protein was sequenced from DNA obtained
CC   from brain tissue contg. Alzheimer neurofibrillary tangles. The protein
CC   can be used to make MAb's to the PHF core or nucleotide probes, used to
CC   diagnose Alzheimer's disease. The protein sequence QIVYKP (AAs 218-223)
CC   was used to design the probes.
CC   See also N91707.
SQ   Sequence 352 AA;

Query Match   74.9%; Score 1719.5; DB 1; Length 352;
Best Local Similarity   78.6%;
Matches 348; Conservative   0; Mismatches   2; Indels 93; Gaps   4;

Qy   1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE 58
          |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   1 MAEPRQEFEVMEDHAG--TYGLGDRKDQGGYTMHQDEGDTDAGLK---------- 44

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
          ||||||||||||||||||||||||| -------AEEAGIGDTPSLEDEA
Db   45 ------------------------------------AEEAGIGDTPSLEDEA 60

Qy   119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 120

Qy   179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 238
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 180

Qy   239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
          |||||||||||||||||||||||||||||||||||||||||-------------------
Db   181 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGK--------------------- 216

Qy   299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   217 -----VQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 269

Qy   359 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   270 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 329

Qy   419 MVDSPQLATLADEVSASLAKQGL 441
          |||||||||||||||||||||||
Db   330 MVDSPQLATLADEVSASLAKQGL 352

RESULT 6

R32708
ID   R32708 standard; protein; 352 AA.
AC   R32708;
DT   15-JUN-1993 (first entry)
DE   Human tau-protein.
KW   Alzheimer's disease; diagnosis; subtyping; monitoring; assay.
OS   Homo sapiens.
PN   WO9303369-A.
PD   18-FEB-1993.
PF   03-AUG-1992; U06382.

PR   01-AUG-1991; US-738778.
PA   (VOOR/) VOORHEIS P H.
PI   Voorheis PH;
DR   WPI; 93-076670/09.
DR   N-PSDB; Q37305.
PT   Method for diagnosing, subtyping and monitoring Alzheimer's
PT   disease - by assaying a sample of body fluid for the presence of a
PT   tau-peptide using an anti-tau antibody
PS   Disclosure: Fig 1; 43pp; English.
PT   The sequence is that one form of human tau protein (from Goedert
PT   et al., PNAS USA 85; 4051-4055) which was used for the prodn.
CC   of anti-tau peptide antibodies. These are used as part of a method
CC   for diagnosing, subtyping or monitoring Alzheimer's disease by
CC   assaying a sample of body fluid for the presence of a tau-peptide
CC   using an anti-tau antibody or the presence of an anti-tau-peptide
CC   autoantibody. The methods can be used for confirming a clinical
CC   diagnosis of Alzheimer's disease and in following the course of the
CC   disease and treatment.
SQ   Sequence ,352 AA;

Query Match   74.9%;   Score 1719.5;   DB 1;   Length 352;
Best Local Similarity   78.6%;   Pred. No. 1.3e-112;
Matches 348; Conservative   0; Mismatches   2; Indels 93; Gaps   4;

Qy   1 MAEPRQEEVEMEDHAGQDTYGLQDRKDQGGYTMH--QEGDTDAGLRESPLQTPEDGSEE   58
         ||||||||||||||||| |||||||||||||
Db   1 MAEPRQEEVEMEDHAG--TYGLQDRKDQGGYTMHQDQEGDTDAGLK----------   44

Qy   59 PGGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
                                                      |||||||||||||
Db   45 ---------------------------------------AEEAGIGDTPSLEDEA   60

Qy 119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 120

Qy 179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 238
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db 121 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTASLPTPPTREPKKVAVVRTPPKSASS 180

Qy 239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGK-------------------- 216

Qy 299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 217 ------VQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 269

Qy 359 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 270 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 329

Qy 419 MVDSPQLATLADEVSASLAKQGL 441
         ||||||||||||||||||||||
Db 330 MVDSPQLATLADEVSASLAKQGL 352

PT   Diagnostic agents for detecting neuroblastoma specific isoform of
PT   microtubule-associated protein - for diagnosis or monitoring of
PT   neuroblastoma, are primers, probes or antibodies, also new
PT   therapeutic antisense sequence
PS   Disclosure: Page ; 34pp; English.
CC   This is a 250 KD isoform of the human microtubule-associated protein 2
CC   (MAP2). This isoform (NB-MAP2) is indicative of neuroblastoma. This
CC   isoform NB-MAP2 arises from alternative splicing of the primary MAP2
CC   transcripts. Diagnostic agents for detecting NB-MAP2 in cells can be
CC   provided so as to detect and monitor neuroblastoma. The diagnostic
CC   agents are pairs of primers for specific amplification of DNA
CC   corresponding to at least part of the MAP2 transcript, provided neither
CC   primer binds to a sequence downstream of nucleotide 4168 or upstream of
CC   nucleotide 4510 of the present 5.5 kb sequence, or the corresponding
CC   antisense sequence, an oligonucleotide that binds to NB-MAP2-specific
CC   mRNA or the corresponding DNA in which nucleotides 4168 and 4510 are
CC   next to one another, an antibody specific for an epitope generated by
CC   translation of the region comprising the splice junction of NB-MAP2
CC   specific mRNA, and a cDNA probe obtained by nick-translation or random
CC   priming of DNA or RNA specific for NB-MAP and obtainable from tissue or
CC   cell probes. The primers are used to detect MAP2-specific dimorphisms in
CC   tissue and cells by polymerase chain reaction (PCR) analysis. The
CC   oligonucleotide and the probes are used to detect NB-MAP2 specific
CC   transcripts (particularly by binding to membrane-bound mRNA) and the
CC   antibodies are used to detect NB-MAP2 in tissue and cells. Specifically
CC   these tests are used to detect neuroblastoma (or its precursor cells)
CC   and to monitor the success of bone marrow purging. The probes can detect
CC   bone marrow and lung metastases in cases where histopathological
CC   diagnosis of neuroblastoma is difficult. The oligonucleotide is used
CC   therapeutically to inhibit NB-MAP2 expression, resulting in development
CC   of neuroblastoma to normal ganglioneurons.
CC   Note: This sequence does not appear in the specification; it has been
CC   made by modifying the human MAP2 sequence provided in Fig 2.
SQ   Sequence 1717 AA;

Query Match   32.2%;   Score 739;   DB 1;   Length 1717;
Best Local Similarity   38.7%;   Pred. No. 2e-43;
Matches 182; Conservative   57; Mismatches 105; Indels 126; Gaps   13;

Qy   48 LQTPIEDGSEEPGS---------------EISDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPE   99
         |||:||| ||:||||||||||||||||||||||| |||||||||||
Db 1291 VQTTDEG--ESGSHSVRFAALEQPEVERRPSPHDEEFEFEVEEAA---EAQAEPKDGSPE 1345

Qy 100 GTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDK--------------- 140
         |||||||||||||||||
Db 1346 APASPE--------------REEVALSEXVTETVDDYKDETTIDDSIMDADSLWVDTQAAGGESA 1396

Qy 141 --------RAKGADGKTKIATPRGAAP-------PGQKG-----------QANAT 169
         :||:| :||
Db 1397 LAPSVFKQAXDKVSDGVTKSPEKRSSLPRPSSILPPRRGVSGDRDENSFSLNSSISSSAR 1456

Qy 170 RIPAKTP------------PARKTPPSS----GEPPKSGDRSGYSSPGSPGTPGSRSRTPSLP 216
         || ||:||
Db 1457 RTTRSEPIRRAGKSGTSTPTTPGSTAITPGTPPSYSSR----TPGTPGTP--SYPRTPHTP 1511

Qy 217 TPP--------TREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPG 271
         ||| ||||||||
Db 1512 GTPKSAILVPSEKVAIIRPPKSPGLTPRQLRLINQPLPDLKNVKSKIGSTDNIKYQPX 1571

Qy 272 GGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHK 331
         |:||:||||:||||||||
Db 1572 GGVQIVTKKIDLSH-----------------------------VISKCGSLKNIRHR 1600

Qy 332 PGGGQVEVKSEKLDFKDRVQSKIGSLGNITHVPGGGNKKIETHKLTFRENAKAKTDHGAE 391
         |||||:::|| |||:||||| :|||||| ||||||:|||||||||||||::||||||
Db 1457 ...

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Db      1601  PGGGRVKIESVKLDFKEKAQAKVGSLDNAHHVPGGGNVKIDSQKLNFREHAKARVDHGAE 1660

Qy       392  IVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL 441
               || :|| ||||||||||||||||::|||||||:|:|:||||||||
Db      1661  IITQSPGRSSVASPRRLSNVSSSGSINLESPQLATLAEDVTAALAKQGL 1710

RESULT   8

ID       W05285  standard; Protein; 140 AA.
AC       W05285;
DT       20-DEC-1996 (first entry)
DE       Human tau protein core sequence.
DE       Tau protein; inhibition; modulation; prophylaxis; treatment;
KW       Alzheimer's disease; motor neurone disease; Lewy body disease;
KW       progressive supranuclear palsy; Pick's disease; ss.
OS       Homo sapiens.
PN       WO9630766-A1.
PD       03-OCT-1996.
PD       25-MAR-1996.
PR       27-MAR-1995; GB-006197.
PA       (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PI       Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
DR       WPI; 96-455570/45.
PT       Assay for inhibitors of tau-tau interaction - used for identifying
PT       cpds., partic. phenothiazine cpds., for treating pathological
PS       Disclosure; Page 56; 97pp; English.
PT       Detecting an agent which modulates or inhibits tau-tau protein
CC       association comprises contacting two tau proteins, distinct from
CC       each other yet capable of binding to the other and where one of the
CC       tau proteins is labelled, in the presence of the agent suspected of
CC       being capable of modulating or inhibiting tau-tau interaction.
CC       Agents identified as being modulators or inhibitors of tau-tau
CC       interaction may be used for the prophylaxis and treatment of
CC       Alzheimer's disease, motor neurone disease, Lewy body disease,
CC       Pick's disease or progressive supranuclear palsy.
SQ       Sequence 140 AA;

Query Match             31.9%;  Score 733;  DB 1;  Length 140;
Best Local Similarity   100.0%; 
Matches  140;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       252  DLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYK 311
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1  DLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYK 60

Qy       312  PVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKI 371
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61  PVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKI 120

Qy       372  ETHKLTFRENAKAKTDHGAE 391
               ||||||||||||||||||||
Db       121  ETHKLTFRENAKAKTDHGAE 140

RESULT   9

ID       W23329  standard; Protein; 1831 AA.
AC       W23329;
DT       23-MAR-1998 (first entry)
DE       Microtubule-associated protein 2 (MAP2).
DE       microtubule-associated protein 2; MAP2; neuroblastoma; human;
KW       isoform; diagnosis; antibody; PCR primer; probe.
OS       Homo sapiens.
PN       WO9727323-A1.
PD       31-JUL-1997.
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FT   Key            Location/Qualifiers
FT   Misc_difference 1825
FT                   /note= "encode by TGA"
FT   Misc_difference 1830
FT                   /note= "encoded by TAG"
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PF       23-JAN-1997; E00320.
PR       23-JAN-1996; EP-100930.
PA       (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PI       Kirsch J, Kurek R;
DR       WPI; 97-393707/36.
N-PSDB;  T64850.
PT       Diagnostic agents for detecting neuroblastoma specific isoform of
PT       microtubule-associated protein - for diagnosis or monitoring of
PT       neuroblastoma, are primers, probes or antibodies, also new
PT       therapeutic antisense sequence.
PS       Disclosure; Fig 2; 34pp; English.
CC       This is the human microtubule-associated protein 2 (MAP2). A 250 kD
CC       isoform of this 270 kD MAP2 is indicative of neuroblastoma. This isoform
CC       NB-MAP2 arises from alternative splicing of the primary MAP2 transcripts.
CC       Diagnostic agents for detecting neuroblastoma. The diagnostic agents are
CC       to detect and monitor neuroblastoma. The diagnostic agents are pairs of
CC       primers for specific amplification of DNA corresponding to at least part
CC       of the MAP2 transcript, provided neither primer binds to a sequence
CC       downstream of nucleotide 4168 or upstream of nucleotide 4510 of the
CC       present 5.5 kb sequence, or the corresponding antisense sequence, an
CC       oligonucleotide that binds to NB-MAP2-specific mRNA or the corresponding
CC       DNA in which nucleotides 4168 and 4510 are next to one another, an
CC       antibody specific for an epitope generated by translation of the region
CC       comprising the splice junction of NB-MAP2 specific mRNA, and a cDNA probe
CC       obtained by nick-translation or random priming of DNA or RNA specific for
CC       NB-MAP and obtainable from tissue or cell probes. The primers are used to
CC       detect MAP2-specific dimorphisms in tissue and cells by polymerase chain
CC       reaction (PCR) analysis. The oligonucleotide and the probes are used to
CC       detect NB-MAP2 specific transcripts (particularly by binding to membrane-
CC       bound mRNA) and the antibodies are used to detect neuroblastoma in tissue and
CC       cells. Specifically these tests are used to detect neuroblastoma (or its
CC       precursor cells) and to monitor the success of bone marrow purging. The
CC       probes can detect bone marrow and lung metastases in cases where
CC       histopathological diagnosis of neuroblastoma is difficult. The
CC       oligonucleotide is used therapeutically to inhibit NB-MAP2 expression,
CC       resulting in development of neuroblastoma to normal ganglioneurons.
SQ       Sequence 1831 AA;

Query Match             31.1%;  Score 713.5;  DB 1;  Length 1831;
Best Local Similarity   36.5%;  Pred. No. 1.3e-41;
Matches  189;  Conservative   73;  Mismatches 137;  Indels 119;  Gaps 18;

Qy         2  AEPRQEFEYMEDHAGQDTYGLGDRKDQ------GGYTMHQEG------DTDAGLKSPLQT-P 51
               |:|          |: |:|   |:|:|                      :||||:||:| |
Db      1348  ASPERE-EVALSEYKTETY--DDYRDETTIDDSIMDADSLWVDTQDDDRSIMTEQLETIP 1404

Qy        52  TEDGSEEPGSEITSPAK------------------STP-----IAEDVIAPLVDE-----GAPGKQA 89
               :| :||                             ::|:     |     :|: |
Db      1405  KEEKAEKEARRSSLEKHRKEKPKTGRGRISTEPERKVARKEPSTVSRDEVRRKAVYKKA 1464

Qy        90  AAQPHTEIPEGTTAEEAGICDTPSLEDEAAGHVTQARMVSKSKDGTGS-------DDKKAK 143
               |: |                :|     |:  |        ||| |:
Db      1465  ELAKKTEVQAHSPSRKFIL--KPAIKYTRPTHLSCVKRKTTAAGGESALAPSVFKQAKDK 1522

Qy       144  GADGKTKIAIPRGAAP-------PGQKG------------------QANATRIPAKTP---- 176
                         | |              |:                     |  :|  | |
Db      1523  VSDGVTKSPEKRSSLPRPSSILPRRGVSGDRDENSFSLNSSSISSSAARRTRSEPIRRAG 1582

Qy       177  ----PAPKTPPSS----GEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPP----TREP 223
                   |       |:        | | || |    |  |:      ||:
Db      1583  KSGTSTPTPGSTAITPGTPPSYSSSR-----TPGTPGTP-SYPRIPHTGTPKSAILVPSE 1637

Qy       224  KKVAVVRTPPKSPSSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLD 283
               ||| ::  |||||:  |||:|  |  | ||||||||||||||||||||||||||||||
Db      1638  KKVAIIRTPPKSPGLTPKQLRLINQPLPDLKNVKSKIGSTDNIKYQPKGGQVQIVTKKID 1697

Qy       284  LSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEK 343
               ||||||||||||:||||||| ||| |||||||||:|||||||||||||||||||||||||
Db      1698  LSH------------------VTSKCGSLKNIRHRPGGGRVKIESVK SPVVSGDT 1726

Qy       344  LDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDT 403
               ||||: :|:|| |||||| || ||| ||||:|| ||||||||||||||| :|| ||||
Db      1726  LDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDT 1831
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Db 1727 LDFKEKAQAKVGSLDNAHHVPGGGNVKIDSQKLNFREHAKARVDHGAEIIIQSPGRSSVA 1786
        |||||||||||||:|||||:||||||||:||:|||||||
Qy 404  SPRLSNVSSGTGSIDMVDSPQLATLADEVSASLAKQGL 441
        |||||||||||:|||||:|||||||:||:|||||||
Db 1787 SPRLSNVSSGSINLLESPQLATLAEDVTAALAKQGL 1824

RESULT 10
ID   R76937 standard; Peptide; 112 AA.
AC   R76937;
DT   04-DEC-1995 (first entry)
DE   PHF-tau (143-254) peptide.
KW   PHF-tau; paired helical filament tau protein; monoclonal antibody;
KW   MAb; phosphorylation; neurological disease; Alzheimer disease;
OS   cerebrospinal fluid.
OS   Homo sapiens.
PN   WO9517429-A.
PD   29-JUN-1995;
PF   14-DEC-1994; E04146.
PR   21-DEC-1993; EP-403133.
PA   (INNO-) INNOGENETICS NV.
PI   Van De Voorde A, Vandermeeren M, Vanmechelen E;
DR   WPI; 95-240616/31.
PT   Novel monoclonal antibodies specific for abnormally phosphorylated
PT   paired helical filament tau protein (PHF-Tau) - useful for post
PT   mortem or in vitro detection of neurological diseases eg. Alzheimer's
PT   disease
PS   Claim 1; Page 44; 57pp; English.
CC   Novel MAbs At180 and AT270 (ECACC 92122204, 93070774) form
CC   immunological complexes with a phosphorylated epitope, given in
CC   R76937, of abnormally phosphorylated tau protein (PHF-tau). The
CC   MAbs are used to specifically detect PHF-tau in cerebrospinal fluid.
SQ   Sequence 112 AA;

Query Match          25.8%; Score 593; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 9.3e-35;
Matches 112; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy 143 KGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGS 202
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1   KGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGS 60

Qy 203 PGSRSRRPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLK 254
       |||||||||||||||||||||||||||||||||||||||||||||||||
Db 61  PGSRSRRPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLK 112

RESULT 11
ID   R92516 standard; peptide; 106 AA.
AC   R92516;
DT   20-SEP-1996 (first entry)
DE   Microtubule-associated tau protein epitope corresp. to pos. 146-251.
KW   Epitope; microtubule-associated protein; tau; phosphorylation; subclass;
KW   paired helical fibre; neurofibrillary tangle; dementia; neurological;
KW   Alzheimer's disease; monoclonal antibody; brain; pathology.
OS   Synthetic.
PN   WO9604309-A1.
PD   15-FEB-1996;
PF   31-JUL-1995; E03032.
PR   29-JUL-1994; EP-870131.
PA   (INNO-) INNOGENETICS NV.
PI   Van DE VOORDE A, Vanmechelen E;
     WPI; 96-129338/13.
PT   Monoclonal antibodies specific for phosphorylated tau - for improved
PT   detection and diagnosis of e.g. Alzheimer's Disease
PS   Claim 2; Page 32; 42pp; English.
CC   This is the amino acid of an epitope derived from the microtubule-
CC   associated tau protein. The phosphorylated subclass of tau protein
CC   from which this epitope originates, forms a major part of the paired
CC   helical fibres which make up neurofibrillary tangles seen in patients

CC   suffering from dementia e.g. Alzheimer's disease. The epitope is esp.
CC   isolated from patients who have recently died from Alzheimer's disease.
CC   It is used to generate monoclonal antibodies for the in vitro detection
CC   or diagnosis of brain/neurological diseases such a Alzheimer's disease
CC   or other diseases where neurofibrillary tangles are a pathological
CC   symptom.
SQ   Sequence 106 AA;

Query Match          24.5%; Score 563; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 106; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy 146 DGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGT 205
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1   DGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGT 60

Qy 206 PGSRSRRPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMP 251
       ||||||||||||||||||||||||||||||||||||||||||||||
Db 61  PGSRSRRPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMP 106

RESULT 12
ID   W05286 standard; Protein; 140 AA.
AC   W05286;
DT   20-DEC-1996 (first entry)
DE   Fragment of microtubule associated protein.
KW   Tau protein; inhibition; modulation; prophylaxis; treatment;
KW   Alzheimer's disease; motor neurone disease; Lewy body disease;
KW   progressive supranuclear palsy; Pick's disease; ss.
OS   Mus musculus.
PN   WO9630766-A1.
PD   03-OCT-1996;
PF   25-MAR-1996; E01307.
PR   27-MAR-1995; GB-006197.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PI   Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
DR   WPI; 96-455570/45.
PT   Assay for inhibitors of tau-tau interaction - used for identifying
PT   cpds., partic. phenothiazine cpds., for treating pathological
PT   tau-tau or neuro-filament aggregation
PS   Disclosure; Page 57; 97pp; English.
CC   Detecting an agent which modulates or inhibits tau-tau protein
CC   association comprises contacting two tau proteins, distinct from
CC   each other yet capable of binding to the other and where one of the
CC   tau proteins is labelled, in the presence of the agent suspected of
CC   being capable of modulating or inhibiting tau-tau interaction.
CC   Agents identified as being modulators or inhibitors of tau-tau
CC   interaction may be used for the prophylaxis and treatment of
CC   Alzheimer's disease, motor neurone disease, Lewy body disease,
CC   Pick's disease or progressive supranuclear palsy. Microtubule
CC   associated proteins share sequence similarity with the human tau
CC   protein in the tandem repeat region.
SQ   Sequence 140 AA;

Query Match          24.0%; Score 551; DB 1; Length 140;
Best Local Similarity 72.1%; Pred. No. 1e-31;
Matches 101; Conservative 22; Mismatches 17; Indels  0; Gaps  0;

Qy 252 DLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYK 311
       |||||||||||||| |:|||:|||:|| |||::||:|||:|||||||||| ||||:|||: |
Db 1   DLKNVKSKIGSTENIKYQPKGGQVRILNKKIDFSKVQSRCGSKDNIKHSAGGGNVQIVTK 60

Qy 312 PVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNIThVPGGGNKKI 371
        :||| |||||||||| || |:|||||:|:| |||:|:|||:|| |||| : ||||||:|:||
Db 61  KIDLSHVTSKCGSLKNIRHRPGGGRVKIESVKLDFREKVQAKVGSLDNAAHVPGGGNVKI 120

Qy 372 ETHKLTFRENAKAKTDHGAE 391
         || ||:||:|||:|||||
Db 121 DSQKLNFREHAKARVDHGAE 140
```

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RESULT 13
W05284
ID   W05284 standard; protein; 95 AA.
AC   W05284;
DT   20-DEC-1996   (first entry)
DE   Human tau protein core fragment.
KW   Tau protein; inhibition; modulation; prophylaxis; treatment;
KW   Alzheimer's disease; motor neurone disease; Lewy body disease;
KW   progressive supranuclear palsy; Pick's disease.
OS   Homo sapiens.
PN   WO9630766-A1.
PD   03-OCT-1996.
PF   25-MAR-1996; E01307.
PR   27-MAR-1995; GB-006197.
PA   (HOFF) HOFFMANN LA ROCHE & CO AG F.
PI   Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
DR   WPI; 96-455570/45.
DR   N-PDB; T39592.
PT   Assay for inhibitors of tau-tau interaction - used for identifying
PT   cpds., partic. phenothiazine cpds., for treating pathological
PT   tau-tau or neuro:filament aggregation
PS   Disclosure; Figure 22; 97pp; English.
CC   Detecting an agent which modulates or inhibits tau-tau protein
CC   association comprises contacting two tau proteins, distinct from
CC   each other yet capable of binding to the other and where one of the
CC   tau proteins is labelled, in the presence of the agent suspected of
CC   being capable of modulating or inhibiting tau-tau interaction.
CC   Agents identified as being modulators or inhibitors of tau-tau
CC   interaction may be used for the prophylaxis and treatment of
CC   Alzheimer's disease, motor neurone disease, Lewy body disease,
CC   Pick's disease or progressive supranuclear palsy.
SQ   Sequence 95 AA;

Query Match             21.8%;  Score 501;  DB 1;  Length 95;
Best Local Similarity   100.0%;  Pred. No. 1.9e-28;
Matches    95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        297 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 60

Qy        357 LDNITHVPGGGNKIETHKLTFRENAKAKTDHGAE 391
              ||||||||||||||||||||||||||||||||||
Db         61 LDNITHVPGGGNKIETHKLTFRENAKAKTDHGAE 95


RESULT 14
R59837
ID   R59837 standard; peptide; 67 AA.
AC   R59837;
DT   04-MAR-1995   (first entry)
DE   Sequence of human microtubule-associated protein tau.
KW   Tau protein; brain; cerebral cortex; hybridoma ECACC 9210853;
KW   Alzheimer's disease; monoclonal antibody; paired helical filament.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   10-DEC-1993; E03499.
PR   14-DEC-1992; EP-403403.
PA   (INNO-) INNOGENETICS NV SA.
PI   Mercken M, Van De Voorde A, Vandermeeren M, Vanmechelen E;
DR   WPI; 94-234211/28.
PT   Monoclonal antibody reactive with tau protein - used to develop
PT   prods. for detection of brain diseases involving tau or paired
PT   helical filaments esp. Alzheimer's disease
PS   Claim 6; Page 38; 52pp; English.
CC   Monoclonal antibody (PHF) tau was partially purified from
CC   postmortem tissue, consisting mostly of grey matter from the frontal
CC   and temporal cortex obtd. from Alzheimer patients. The tissue
CC   was homogenised with 10 vols of cold buffer (10mM Tris, 1mM EGTA,
CC   0.8M NaCl, 10% sucrose, pH 7.4). After centrifugation for 20 mins at
CC   4 degrees C, the supernatant was adjusted to 1% (wt/vol) N-
CC   lauroylsarcosine and 1% (vol/vol) 2-mercaptoethanol and incubated
CC   while rotating on a mixer for 2.5 hrs at 37 degrees C. The mixt. was
CC   centrifuged at 108,000 g for 35 mins at 20 degrees C. The PHF-tau
CC   concg. pellet was washed with PBS and resuspended in 1ml of the same
CC   buffer. Hybridomas which produced MAbs reactive with tau protein
CC   were obtd. from the spleen cells of Balb/C mice primed s.c. with
CC   partially purified PHF. A MAb which forms an immunological complex
CC   with a human tau protein of sequence in R59837 is secreted by the
CC   hybridoma deposited at ECACC on Oct. 8 1992 under No. 92100853.
SQ   Sequence 67 AA;

Query Match             15.9%;  Score 364;  DB 1;  Length 67;
Best Local Similarity   100.0%;  Pred. No. 4.4e-19;
Matches    67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        155 RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPS 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPS 60

Qy        215 LPTPPTR 221
              |||||||
Db         61 LPTPPTR 67


RESULT 15
W34876
ID   W34876 standard; peptide; 55 AA.
AC   W34876;
DT   27-MAR-1998   (first entry)
DE   Human tau protein fragment.
KW   Antibody; phosphorylated tau protein; paired helical filament;
KW   detection; Alzheimer's disease; human.
OS   Homo sapiens.
PN   WO9734145-A1.
PD   18-SEP-1997.
PF   13-MAR-1997; J00804.
PR   13-MAR-1996; JP-056090.
PA   (MITU) MITSUBISHI CHEM CORP.
PI   Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
DR   WPI; 97-470978/43.
PT   Antibody prepared using a partial peptide containing part of
PT   phosphorylated tau protein - used for detecting Alzheimer's disease
PS   Example; Page 37; 48pp; Japanese.
CC   An antibody, prepared using a partial peptide containing the
CC   phosphorylated residue of the phosphorylated tau protein, e.g. the
CC   present sequence, in a paired helical filament, can be used to
CC   detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC   protein in brain extracts or tissue fragments.
SQ   Sequence 55 AA;

Query Match             11.8%;  Score 270;  DB 1;  Length 55;
Best Local Similarity   100.0%;  Pred. No. 1.2e-12;
Matches    55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        384 AKTDHGAEIYVKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAK 438
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Db          1 AKTDHGAEIYVKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAK 55


Search completed: September 28, 2000, 19:58:13
Job time: 10516 sec
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                    GenCore version 4.5
                    Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        September 28, 2000, 18:46:58 ; Search time 41.36 Seconds
                                             (without alignments)
                                             163.447 Million cell updates/sec

Title:         US-09-142-613-1
Perfect score: 2295
Sequence:      1 MAEPRQEEVMEDHAGQDTIY.........SPQLATLADEVSASLAKQGL 441

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      152396 seqs, 15329161 residues

Total number of hits satisfying chosen parameters:        152396

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Issued_Patents_AA:*
               1: /cgn1_7/ptodata/1/1aa/5A_COMB.pep:*
               2: /cgn1_7/ptodata/1/1aa/5B_COMB.pep:*
               3: /cgn1_7/ptodata/1/1aa/6_COMB.pep:*
               4: /cgn1_7/ptodata/1/1aa/PCTUS.COMB.pep:*
               5: /cgn1_7/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	1735.5	75.6	352	2	US-08-726-306A-17	Sequence 17, Appl
2	1735.5	75.6	391	2	US-08-244-951A-10	Sequence 10, Appl
3	1735.5	75.6	391	2	US-08-389-011-23	Sequence 23, Appl
4	1735.5	75.6	391	2	US-08-403-917A-23	Sequence 23, Appl
5	1731.5	75.4	351	1	US-08-159-969-2	Sequence 2, Appl
6	593	25.8	112	2	US-08-666-360-1	Sequence 1, Appl
7	416	18.1	160	2	US-08-726-306A-35	Sequence 35, Appl
8	364	15.9	67	2	US-08-726-306A-1	Sequence 1, Appl
9	364	15.9	67	2	US-08-389-011-1	Sequence 1, Appl
10	339	14.8	67	2	US-08-403-917A-1	Sequence 1, Appl
11	198	8.6	67	3	US-08-244-951A-1	Sequence 1, Appl
12	185	8.1	40	2	US-08-726-306A-65	Sequence 65, Appl
13	185	8.1	34	2	US-08-602-264A-10	Sequence 10, Appl
14	174	7.6	33	2	US-08-461-018A-10	Sequence 10, Appl
15	174	7.6	33	2	US-08-389-011-2	Sequence 2, Appl
16	174	7.6	35	2	US-08-403-917A-2	Sequence 2, Appl
17	172.5	7.5	455	4	PCT-US93-07261-13	Sequence 13, Appl
18	172.5	7.5	1663	4	PCT-US93-07261-16	Sequence 16, Appl
19	165	7.2	33	2	US-08-244-951A-16	Sequence 16, Appl
20	164	7.1	31	2	US-08-714-481-2	Sequence 2, Appl
21	157	6.8	984	1	US-08-242-932-2	Sequence 2, Appl
22	157	6.8	984	1	US-08-242-932-4	Sequence 4, Appl
23	157	6.8	984	1	PCT-US95-06111-2	Sequence 2, Appl
24	157	6.8	984	1	US-08-714-481-10	Sequence 10, Appl
25	150	6.5	1187	3	US-08-545-860D-28	Sequence 28, Appl
26	150	6.5	1187	3	US-08-320-559-28	Sequence 28, Appl
27	150	6.5	1210	1	US-08-320-559-26	Sequence 26, Appl
28	150	6.5	1210	3	US-08-545-860D-26	Sequence 26, Appl
29	150	6.5	1210	4	PCT-US94-04496-26	Sequence 26, Appl
30	146	6.4	1780	1	US-08-769-309A-5	Sequence 5, Appl
31	142	6.2	907	3	US-08-783-774-2	Sequence 2, Appl
32	142	6.2	907	4	PCT-US95-04611A-19	Sequence 19, Appl
33	142	6.2	1057	2	US-08-931-820-4	Sequence 4, Appl
34	140.5	6.1	478	3	US-08-155-888-2	Sequence 2, Appl
35	140.5	6.1	1706	2	US-08-459-568-2	Sequence 2, Appl
36	140.5	6.1	1706	2	US-08-399-411-2	Sequence 2, Appl
37	140.5	6.1	1706	3	US-08-516-859A-2	Sequence 2, Appl
38	140	6.1	1057	3	US-08-931-820-1	Sequence 1, Appl
39	139.5	6.1	1442	2	US-08-316-650-10	Sequence 10, Appl
40	139.5	6.1	1442	4	PCT-US93-07261-11	Sequence 11, Appl
41	139.5	6.1	1588	4	PCT-US95-02251-12	Sequence 12, Appl
42	137	6.0	27	2	US-08-405-175A-5	Sequence 5, Appl
43	136.5	5.9	335	2	US-08-244-951A-6	Sequence 6, Appl
44	136.5	5.9	682	1	US-08-642-255-126	Sequence 126, App
45	136.5	5.9	682	1	US-08-397-633A-36	Sequence 36, Appl

ALIGNMENTS

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RESULT 1
US-08-726-306A-17
Sequence 17, Application US/0872630 6A
Patent No. 5958684
GENERAL INFORMATION:
; APPLICANT: van Leeuwen, Frederik Willem
; APPLICANT: Burbach, Johannes Peter Henri
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Banner & Witcoff, Ltd.
;  STREET: 1 Financial Center
;  CITY: Boston
;  STATE: MA
;  COUNTRY: US
;  ZIP: 02111
; COMPUTER READABLE FORM:
;  MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/726,306A
;  FILING DATE: 02-Oct-1996
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: GB 95/20080.4
;  FILING DATE: 02-Oct-1995
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 60/009,832
;  FILING DATE: 01-Jan-1996
; ATTORNEY/AGENT INFORMATION:
;  NAME: Williams, Ph.D., Kathleen M.
;  REGISTRATION NUMBER: 34,380
;  REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
; TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (617) 345-9100
;  TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 17:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 352 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: unknown
;  MOLECULE TYPE: protein
; US-08-726-306A-17

Query Match         75.6%;  Score 1735.5;  DB 2;  Length 352;
Best Local Similarity  79.0%;  Pred. No. 1.4e-123;
Matches  350;  Conservative  0;  Mismatches  0;  Indels  93;  Gaps  4;
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Qy     1  MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE  58
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Db     1  MAEPRQEFEVMEDHAG--TYGLGDRKDQGGYTMHQDQEGDTDAGLK------------  44

Qy    59  PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA  118
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    45  ------------------------------------------AEEAGIGDTPSLEDEA  60

Qy   119  AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA  178
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Db    61  AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA  120

Qy   179  PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS  238
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS  180

Qy   239  AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK  298
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGK--------------------  216

Qy   299  HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD  358
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Db   217  ------VQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD  269

Qy   359  NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID  418
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   270  NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID  329

Qy   419  MVDSPQLATLADEVSASLAKQGL  441
          |||||||||||||||||||||||
Db   330  MVDSPQLATLADEVSASLAKQGL  352
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RESULT 2
US-08-244-951A-10
; Sequence 10, Application US/08244951A
; Patent No. 5843779
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BIERMAN & MUSERLIAN
;   STREET: 600 THIRD AVENUE
;   CITY: NEW YORK
;   STATE: NEW YORK
;   COUNTRY: USA
;   ZIP: 10016
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: FLOPPY DISK
;   COMPUTER: IBM PC COMPATIBLE
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/244,951A
;   FILING DATE: 19-JAN-1995
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/EP93/03499
;   FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP/92/403403.6
;   FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: CHARLES A. MUSERLIAN
;   REGISTRATION NUMBER: 19,683
;   REFERENCE/DOCKET NUMBER: 410.003A

; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 661-8000
;   TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 391
;   TYPE: Amino Acid
;   STRANDEDNESS: Unknown
;   TOPOLOGY: Unknown
;   FEATURE:
;   NAME/KEY: mTHFMPH-tau1 fusion protein
US-08-244-951A-10

Query Match   75.6%; Score 1735.5; DB 2; Length 391;
Best Local Similarity   79.0%; Pred. No. 1.6e-123;
Matches 350; Conservative 0; Mismatches 0; Indels 93; Gaps 4;

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Qy     1  MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE  58
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Db     1  MAEPRQEFEVMEDHAG--TYGLGDRKDQGGYTMHQDQEGDTDAGLK------------  40

Qy    59  PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA  118
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Db    40  MAEPRQEFEVMEDHAG--TYGLGDRKDQGGYTMHQDQEGDTDAGLK------------  83

Qy    59  PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA  118
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Db    84  ------------------------------------------AEEAGIGDTPSLEDEA  99

Qy   119  AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA  178
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Db   100  AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA  159

Qy   179  PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS  238
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Db   160  PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS  219

Qy   239  AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK  298
          |||||||||||||||||||||||||||||||||||
Db   220  AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGK------------------  255

Qy   299  HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD  358
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Db   256  ------VQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD  308

Qy   359  NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID  418
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Db   309  NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID  368

Qy   419  MVDSPQLATLADEVSASLAKQGL  441
          |||||||||||||||||||||||
Db   369  MVDSPQLATLADEVSASLAKQGL  391
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RESULT 3
US-08-389-011-23
; Sequence 23, Application US/08389011
; Patent No. 5861257
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BIERMAN & MUSERLIAN
;   STREET: 600 THIRD AVENUE
;   CITY: NEW YORK
;   STATE: NEW YORK
;   COUNTRY: USA
;   ZIP: 10016
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 391
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-389-011-23

Query Match   75.6%; Score 1735.5; DB 2; Length 391;
Best Local Similarity   79.0%; Pred. No. 1.6e-123;
Matches 350; Conservative 0; Mismatches 0; Indels 93; Gaps 4;

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Qy    1 MAEPRQEFEVMEDHAGQODTYGLGDRKDQGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE 58
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Db   40 MAEPRQEFEVMEDHAG--TYGLGDRKDQGGYTMHQDQEGDTDAGLK-------------- 83

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEFAGIGDTPSLEDEA 118
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Db   84 ------------------------------------------AEEAGIGDTPSLEDEA 99

Qy  119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178
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Db  100 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 159

Qy  179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 238
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Db  160 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 219

Qy  239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
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Db  220 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGK----------------------- 255

Qy  299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358
         |||||||      |||||||||||||||||||||||||||||||||||||||||||
Db  256 -------VQIVKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 308

Qy  359 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  309 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 368

Qy  419 MVDSPQLATLADEVSASLAKQGL 441
         |||||||||||||||||||||||
Db  369 MVDSPQLATLADEVSASLAKQGL 391
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RESULT 4
US-08-403-917A-23
Sequence 23, Application US/08403917A
Patent No. 6010913
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,917A
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 391
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-403-917A-23

Query Match   75.6%; Score 1735.5; DB 3; Length 391;
Best Local Similarity   79.0%; Pred. No. 1.6e-123;
Matches 350; Conservative 0; Mismatches 0; Indels 93; Gaps 4;

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Qy    1 MAEPRQEFEVMEDHAGQODTYGLGDRKDQGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE 58
         ||||||||||||||||  ||||||||||||||||   ||||||||||
Db   40 MAEPRQEFEVMEDHAG--TYGLGDRKDQGGYTMHQDQEGDTDAGLK-------------- 83

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEFAGIGDTPSLEDEA 118
                                                      ||||||||||||||||
Db   84 ------------------------------------------AEEAGIGDTPSLEDEA 99

Qy  119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db 100 AGHVTQARMVSKSKDGTGSDDKKAKAGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 159

Qy 179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKRVAVVRTPPKSPSS 238
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 160 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKRVAVVRTPPKSPSS 219

Qy 239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 220 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGK------------------------ 255

Qy 299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 256 ------VQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 308

Qy 359 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 309 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 368

Qy 419 MVDSPQLATLADEVSASLAKQGL 441
         ||||||||||||||||||||
Db 369 MVDSPQLATLADEVSASLAKQGL 391

RESULT 5
US-08-159-969-2
; Sequence 2, Application US/08159969
; Patent No. 5492812
; GENERAL INFORMATION:
;   APPLICANT: Voorheis, Paul H.
;   TITLE OF INVENTION: Diagnostic Method for Alzheimer's
;   TITLE OF INVENTION: Disease
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/159,969
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/738,778
;   FILING DATE: 01-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Misrock, S.Leslie
;   REGISTRATION NUMBER: 18,872
;   REFERENCE/DOCKET NUMBER: 4697-040
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212 790-9090
;   TELEFAX: 212 869-8864/9741
;   TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 351 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-159-969-2

Query Match   75.4%; Score 1731.5; DB 1; Length 351;
Best Local Similarity   79.0%; Pred. No. 2.8e-123;
Matches 349; Conservative   0; Mismatches   0; Indels   93; Gaps   4;

Qy   1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYIMH--QEGDTDAGLKESPLQTPTEDGSEE 58

Db   1 MAEPRQEFEVMEDHAG--TYGLGDRKDQGGYTMHQDQEGDTDAGLK-------------- 44
         ||||||||||||||||| ||||||||||||||||| ||||||||

Qy   59 PGSETSDAKSTPIAEDVTAPLVDEGAPGKQAAAQPHETEIPEGTTAEEAGIGDTPSLEDEA 118
                                                             ||||||||||
Db   45 --AEEAGIGDTPSLEDEA 60

Qy 119 AGHVTQARMVSKSKDGTGSDDKKAKAGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGHVTQARMVSKSKDGTGSDDKKAKAGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 120

Qy 179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKRVAVVRTPPKSPSS 238
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKRVAVVRTPPKSPSS 180

Qy 239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
         |||||||||||||||||||||||||||||||||||
Db 181 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGK------------------------ 216

Qy 299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 217 ------VQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 269

Qy 359 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 270 NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 329

Qy 419 MVDSPQLATLADEVSASLAKQG 440
         ||||||||||||||||||||||
Db 330 MVDSPQLATLADEVSASLAKQG 351

RESULT 6
US-08-666-360-1
; Sequence 1, Application US/08666360
; Patent No. 6008024
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION: Monoclonal antibodies specific for PHF-tau,
;   TITLE OF INVENTION: hybridomas secreting them, antigen recognition of these
;   TITLE OF INVENTION: antibodies and their applications
;   NUMBER OF SEQUENCES: 3
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/666,360
;   FILING DATE:
;   CLASSIFICATION: 435
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 112 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-666-360-1

Query Match   25.8%; Score 593; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.1e-38;
Matches 112; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 143 KGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGS 202
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 KGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGS 60

Qy 203 PGTPGSRSRTPSLPTPPTREPKRVAVVRTPPKSPSSAKSRLQTAPVPMPDLK 254
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PGTPGSRSRTPSLPTPPTREPKRVAVVRTPPKSPSSAKSRLQTAPVPMPDLK 112

RESULT 7
US-08-726-306A-35
Sequence 35, Application US/0872630 6A
; Patent No. 5558684
GENERAL INFORMATION:
; APPLICANT: van Leeuwen, Frederik Willem
; APPLICANT: Burbach, Johannes Peter Henri
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1 Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,306A
; FILING DATE: 02-Oct-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 95/20080.4
; FILING DATE: 02-Oct-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/009,832
; FILING DATE: 01-Jan-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

US-08-726-306A-35

Query Match   18.1%; Score 416; DB 2; Length 160;
Best Local Similarity   45.1%; Pred. No. 1.4e-24;
Matches   92; Conservative 24; Mismatches 36; Indels 52; Gaps 6;

Qy 161 GOKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSS--PGSPGTPGSRSRTPSLPTP 218
           |:|:| :|| |||||| |||::|||| |||| ||
Db   2 GKSGTPSTPT-TPGSTAIPTGPPPS-----------YSSRTPGTPGTP-SYPRTPHTPGT 47

Qy 219 P-----TREPKVAVVRTPEPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHOPGGG 273
             ||:|||||:||:|||||| ||||||||:|:|||:|:|:||||
Db 48 PKSAILVPSEKKVAIIRTPEPKSPGITPKQLRLINQPLPDLKNVKSKIGSTDNIKYQPKGG 107

Qy 274 KVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIYKPVDLSKVTSKCGSLGNIHHKPG 333
           |:|||:|| |||||||||||||||||||||||:|||
Db 108 QVQIVTKIDLSH--------------------VTSKCGSLKNIRHRPG 136

Qy 334 GGQVEVKSEKLDFKDRVQSKIGSL 357
           ||:|:||:| ||||:| |:|:||
Db 137 GGRVKIESVKLDFKEKAQAVGSL 160

RESULT 8
US-08-389-011-1
; Sequence 1, Application US/08389011
; Patent No. 5861257

GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,011
; FILING DATE: 15-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,916
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: linear

US-08-389-011-1

RESULT 9
US-08-403-917A-1
; Sequence 1, Application US/08403917A
; Patent No. 6010913

Query Match   15.9%; Score 364; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches   67; Conservative   0; Mismatches   0; Indels 0; Gaps 0;

Qy 155 RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPS 214
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPS 60

Qy 215 LPTPPPR 221
           |||||||
Db 61 LPTPPPR 67

GENERAL INFORMATION:
 APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
 APPLICANT: VANMECHELEN, EUGEEN;
 APPLICANT: VAN DE VOORDE, ANDRE
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
 TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
 TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: BIERMAN & MUSERLIAN
  STREET: 600 THIRD AVENUE
  CITY: NEW YORK
  STATE: NEW YORK
  COUNTRY: USA
  ZIP: 10016
 COMPUTER READABLE FORM:
  MEDIUM TYPE: FLOPPY DISK
  COMPUTER: IBM PC COMPATIBLE
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/403,917A
  FILING DATE: 19-JAN-1995
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/256,167
  FILING DATE: 27-JUN-1994
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/244,951
  FILING DATE: 13-JUN-1994
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/EP93/03499
  FILING DATE: 10-DEC-1993
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: EP/92/403403.6
  FILING DATE: 14-DEC-1992
 ATTORNEY/AGENT INFORMATION:
  NAME: CHARLES A. MUSERLIAN
  REGISTRATION NUMBER: 19,683
  REFERENCE/DOCKET NUMBER: 410.003-1
 TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 661-8000
  TELEFAX: (212) 661-8002
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 67
  TYPE: Amino Acid
  STRANDEDNESS: Unknown
  TOPOLOGY: Unknown
US-08-403-917A-1

Query Match   15.9%;   Score 364; DB 3;   Length 67;
Best Local Similarity   100.0%; Pred. No. 3.8e-21;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   155 RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPS 214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPS 60

Qy   215 LPTPPTR 221
          |||||||
Db   61 LPTPPTR 67

RESULT 10
US-08-244-951A-1
; Sequence 1, Application US/08244951A
; Patent No. 5843779
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE

 TITLE OF INVENTION: MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
 TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
 TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: BIERMAN & MUSERLIAN
  STREET: 600 THIRD AVENUE
  CITY: NEW YORK
  STATE: NEW YORK
  COUNTRY: USA
  ZIP: 10016
 COMPUTER READABLE FORM:
  MEDIUM TYPE: FLOPPY DISK
  COMPUTER: IBM PC COMPATIBLE
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/244,951A
  FILING DATE: 19-JAN-1995
  CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/EP93/03499
  FILING DATE: 10-DEC-1993
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: EP/92/403403.6
  FILING DATE: 14-DEC-1992
 ATTORNEY/AGENT INFORMATION:
  NAME: CHARLES A. MUSERLIAN
  REGISTRATION NUMBER: 19,683
  REFERENCE/DOCKET NUMBER: 410.003A
 TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 661-8000
  TELEFAX: (212) 661-8002
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 67
  TYPE: Amino Acid
  STRANDEDNESS: Unknown
  TOPOLOGY: Unknown
 FEATURE:
  NAME/KEY: human tau protein 155-211
US-08-244-951A-1

Query Match   14.8%;   Score 339; DB 2;   Length 67;
Best Local Similarity   92.5%;   Pred. No. 2.9e-19;
Matches 62; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy   155 RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPS 214
          |||||||||||||||||||||||: || ||||||||||||||||||||||||||||||||
Db   1 RGAAPPGQKGQANATRIPAKTPPSEEPPKSGEPPKSGDRSGYSSPGSPGTPGSRSRTPS 60

Qy   215 LPTPPTR 221
          |||||||
Db   61 LPTPPTR 67

RESULT 11
US-08-726-306A-65
; Sequence 65, Application US/08726306A
; Patent No. 5958684
; GENERAL INFORMATION:
; APPLICANT: van Leeuwen, Frederik Willem
; APPLICANT: Burbach, Johannes Peter Henri
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1 Financial Center
; CITY: Boston

STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-726-306A-65

Query Match   8.6%; Score 198; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 391 EIYVKSPVVSGDTSPRHLSNVSSTGSGSIDMVDSPQLATLAD 430
        |||||||||||||||||||||||||||||||||||||||||
Db   1 EIYVKSPVVSGDTSPRHLSNVSSTGSGSIDMVDSPQLATLAD 40

RESULT 12
US-08-602-264A-10
Sequence 10, Application US/08602264A
Patent No. 5837853
GENERAL INFORMATION:
APPLICANT: Akihiko TAKASHIMA et al.
TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF
TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-602-264A-10

Query Match   8.1%; Score 185; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 SGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPK 224
        ||||||||||||||||||||||||||||||||||
Db   1 SGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPK 34

RESULT 13
US-08-461-018A-10
Sequence 10, Application US/08461018A
Patent No. 6071694
GENERAL INFORMATION:
APPLICANT: Akihiko TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,018A
FILING DATE: June 5, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-461-018A-10

Query Match   8.1%; Score 185; DB 3; Length 34;

Qy   191 SGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPK 224
           ||||||||||||||||||||||||||||||||||
Db   1 SGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPK 34

Best Local Similarity 100.0%; Conservative 0; Mismatches 34; Pred. No. 4.9e-08; Indels 0; Gaps 0;

RESULT 14
US-08-389-011-2
; Sequence 2, Application US/08389011
; Patent No. 5861257
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BIERMAN & MUSERLIAN
;   STREET: 600 THIRD AVENUE
;   CITY: NEW YORK
;   STATE: NEW YORK
;   COUNTRY: USA
;   ZIP: 10016
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: FLOPPY DISK
;   COMPUTER: IBM PC COMPATIBLE
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/389,011
;   FILING DATE: 15-FEB-1995
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/403,917
;   FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/403,916
;   FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/244,951
;   FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/EP93/03499
;   FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP/92/403403.6
;   FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: CHARLES A. MUSERLIAN
;   REGISTRATION NUMBER: 19,683
;   REFERENCE/DOCKET NUMBER: 410.003-1-CON
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 661-8000
;   TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 33
;   TYPE: Amino Acid
;   STRANDEDNESS: Unknown
;   TOPOLOGY: Unknown
US-08-389-011-2

Query Match   7.6%; Score 174; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   199 SPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRT 231
           |||||||||||||||||||||||||||||||||
Db   1 SPGSPGTPGSRSRTPSLPTPPTREPK 34

Db   1 SPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRT 33
           |||||||||||||||||||||||||||||||||

RESULT 15
US-08-403-917A-2
; Sequence 2, Application US/08403917A
; Patent No. 6010913
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BIERMAN & MUSERLIAN
;   STREET: 600 THIRD AVENUE
;   CITY: NEW YORK
;   STATE: NEW YORK
;   COUNTRY: USA
;   ZIP: 10016
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: FLOPPY DISK
;   COMPUTER: IBM PC COMPATIBLE
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/403,917A
;   FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/256,167
;   FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/244,951
;   FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/EP93/03499
;   FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP/92/403403.6
;   FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: CHARLES A. MUSERLIAN
;   REGISTRATION NUMBER: 19,683
;   REFERENCE/DOCKET NUMBER: 410.003-1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 661-8000
;   TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 33
;   TYPE: Amino Acid
;   STRANDEDNESS: Unknown
;   TOPOLOGY: Unknown
US-08-403-917A-2

Query Match   7.6%; Score 174; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   199 SPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRT 231
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Db   1 SPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRT 33

Search completed: September 28, 2000, 19:59:08
Job time: 4330 sec

OM protein - protein search, using sw model

GenCore version 4.5
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Run on: September 28, 2000, 18:58:10 ; Search time 47.67 Seconds
                                              (without alignments)
                                              572.502 Million cell updates/sec

Title: US-09-142-613-1
Perfect score: 2295
Sequence: 1 MAEPRQEFEVMEDHAGQDTY..........SPQLATLADEVSASLAKQGL 441

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 178050 seqs, 61884766 residues

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_64:*
                   1: pir:*
                   2: pir2:*
                   3: pir3:*
                   4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2262	98.6	441	1	QRHUT1	microtubule-associ
2	2011.5	87.6	448	1	QRBOT1	microtubule-associ
3	2003.5	87.3	432	2	JS0306	microtubule-associ
4	1861.5	81.1	686	2	A38235	microtubule-associ
5	1821	79.3	733	2	A45301	microtubule-associ
6	1710.5	74.5	374	2	S46264	microtubule-associ
7	1558.5	67.9	316	1	QRHUT2	microtubule-associ
8	1512	65.9	341	1	QRHUT2	microtubule-associ
9	1508	65.7	364	1	B28820	microtubule-associ
10	1493	65.1	402	1	QRBOT2	microtubule-associ
11	746.5	32.5	472	1	I67793	microtubule-associ
12	723	31.5	1830	2	A37981	microtubule-associ
13	719.5	31.4	1828	2	A40115	microtubule-associ
14	717.5	31.3	1825	2	S13507	microtubule-associ
15	713.5	31.1	1824	1	QRHUMT	microtubule-associ
16	710	30.9	323	1	A55983	microtubule-associ
17	546	23.8	381	1	S51375	microtubule-associ
18	545	23.7	1152	1	A33183	microtubule-associ
19	523.5	22.8	1125	2	B41206	microtubule-associ
20	481	21.0	125	2	I52650	microtubule-associ
21	475	20.7	1072	2	A37127	microtubule-associ
22	428.5	18.7	982	2	A53253	microtubule-associ
23	403.5	17.6	1224	1	T14007	microtubule-associ
24	278	12.1	242	1	T16349	hypothetical prote
25	193.5	8.4	1560	2	T02885	peroxisome prolife
26	192	8.4	2187	2	T30826	nascent polypeptid
27	184.5	8.0	1211	2	T42230	AF4 protein - mous
28	183.5	8.0	813	2	S70795	vsaA protein precu
29	179	7.8	3507	2	T34513	hypothetical prote
30	178	7.8	971	2	T19431	hypothetical prote
31	176	7.7	990	2	151618	nucleolar phosphop
32	175.5	7.7	704	2	A42680	nucleolus-cytoplas
33	175.5	7.6	858	2	S15762	neurofilament trip
34	175.5	7.6	2441	2	D71623	erythrocyte membra
35	173	7.5	903	2	T19209	probable protein k
36	172.5	7.5	455	2	S31806	emp3 protein - Pla
37	172	7.5	734	2	B42680	nucleolus-cytoplas
38	172	7.5	744	2	T35192	probable ABC trans
39	171.5	7.5	6642	2	T29757	protein UNC-89 - C
40	169.5	7.4	801	2	T29018	hypothetical prote
41	167.5	7.3	428	2	T24769	hypothetical prote
42	165.5	7.2	839	2	F75518	hypothetical prote
43	165	7.2	1029	2	T30351	mucin-like protein
44	163.5	7.1	825	1	EDBEXD	immediate-early pr
45	163.5	7.1	916	2	A27864	neurofilament trip

ALIGNMENTS

RESULT   1
QRHUT1
microtubule-associated protein tau, long splice form - human
N;Alternate names: microtubule-binding protein tau; neurofibrillary tangle protein tau
N;Contains: microtubule-associated protein tau type II; microtubule-associated protei
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
C;Accession: JS0370; A32217; JN0009; S03796; S26665; S26662; S17302; A43444;
R;Goedert, M.; Spillantini, M.G.; Jakes, R.; Rutherford, D.; Crowther, R.A.
A;Title: Multiple isoforms of human microtubule-associated protein tau: sequences and
#the clone htau24 sequence lacks inserts 1 and 2; the clone htau37 sequence lacks ins
R;Reference number: JS0370; JS0370; MUID:90380393
A;Accession: JS0370
A;Molecule type: mRNA
A;Residues: 1-441 <GOE>
A;Note: six isoforms are found; the clone htau40 sequence is shown. Residues 45-73, 7
Neuron 3, 519-526, 1989
A;Title: Cloning and sequencing of the cDNA encoding a core protein of the paired hel
R;Reference number: A30217; MUID:88234557
A;Accession: A30217
A;Molecule type: mRNA
A;Residues: 1-44,103-274,306-441 <GO2>
A;Cross-references: GB:J03778; NID:g336684; PIDN:AAA60615.1; PID:g338685
R;Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A;Title: The microtubule binding domain of tau protein.
R;Reference number: JN0009; MUID:90180482
A;Accession: JN0009
A;Molecule type: mRNA
A;Residues: 1-44,103-441 <GO3>
A;Cross-references: EMBL:X14474; NID:g36724; PIDN:CAA32636.1; PID:g36725
R;Andreadis, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992
A;Title: Structure and novel exons of the human tau gene.
R;Reference number: S26662; MUID:93041757
A;Accession: S26665
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 144-185 <AND>
A;Cross-references: EMBL:X61372; NID:g36718; PID:g36719
A;Accession: S26666
A;Status: nucleic acid sequence not shown; translation not shown

EMBO J. 8, 393-399, 1989
A;Title: Cloning and sequencing of the cDNA encoding an isoform of microtubule-associ
R;Reference number: S03796; MUID:89251564
A;Accession: S03796
A;Molecule type: mRNA
A;Residues: 1-44,103-274,306-441 <LEE>
R;Goedert, M.; Spillantini, M.G.; Potier, M.C.; Ulrich, J.; Crowther, R.A.
R;Goedert, M.; Wischik, C.M.; Crowther, R.A.; Walker, J.E.; Klug, A.
Proc. Natl. Acad. Sci. U.S.A. 85, 4051-4055, 1988
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

A;Molecule type: DNA
A;Residues: 187-274 <AN2>
A;Cross-references: EMBL:X61374; NID:g36722; PID:g36723
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A;Accession: S26662
A;Molecule type: DNA
A;Residues: 371-441 <ANW>
A;Cross-references: EMBL:X61373
R;Jakes, R.; Novak, M.; Davison, M.; Wischik, C.M.
EMBO J. 10, 2725-2729, 1991
A;Title: Identification of 3- and 4-repeat tau isoforms within the PHF in Alzheimer's di
A;Reference number: S17302; MUID:92077714
A;Accession: S17302
A;Status: preliminary
A;Molecule type: protein
C;Residues: 268-274,306-395 <JAK>
R;Hasegawa, M.; Morishima-Kawashima, M.; Takio, K.; Suzuki, M.; Titani, K.; Ihara, Y.
J. Biol. Chem. 267, 17047-17054, 1992
A;Title: Protein sequence and mass spectrometric analyses of tau in the Alzheimer's dise
A;Reference number: A43444; MUID:92381012
A;Accession: A43444
A;Molecule type: protein
A;Residues: 2-73,103-130,151-180,191-254,260-269,275-290,299-317,322-340,344-347,354-383
A;Cross-references: GDB:119434; OMIM:157140
A;Gene: GDB:MAPT
o;Genetics:
o;Comment: This heterogeneous protein, which is found predominantly in cells of the nerv
C;Comment: This heterogeneous protein, which is found predominantly in cells of the nerv
o;the core protein of the paired helical filament of Alzheimer's disease.
A;Note: sequence extracted from NCBI backbone (NCBIP:112039).
A;Experimental source: Alzheimer's disease brain
A;Map position: 17q21-17q21
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; Alzheimer's disease; microtubule binding;
F;1-441/Product: microtubule-associated protein tau, long splice form #status predicted
F;1-274,306-441/Product: microtubule-associated protein tau (clone htau39) #status predi
F;1-73,103-441/Product: microtubule-associated protein tau (clone htau34) #status predi
F;1-73,103-274,306-441/Product: microtubule-associated protein tau (clone htau37) #statu
F;1-44,103-441/Product: microtubule-associated protein tau, fetal #status predic
F;1-44,103-274,306-441/Product: microtubule-associated protein tau type II #status predicted <MA
F;252-282/Domain: MAP2/tau repeat homology <MT1>
F;283-313/Domain: MAP2/tau repeat homology <MT2>
F;314-344/Domain: MAP2/tau repeat homology <MT3>
F;345-376/Domain: MAP2/tau repeat homology <MT4>

Query Match   98.6%;   Score 2262;   DB 1;   Length 441;
Best Local Similarity   99.1%;   Pred. No. 3.2e-109;
Matches   439;   Conservative   0;   Mismatches   0;   Indels   4;   Gaps   2;

Qy   1 MAERQEFEVMEDHAGQDTYGLGDRKDQGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE 58
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Db   1 MAEPRQEFEVMEDHAG--TYGLGDRKDQGGYTMHQDEGDTDAGLKESPLQTPTEDGSEE 58

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118

Qy   119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178

Qy   179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 238

Qy   239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   239 AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298

Qy   299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358

Qy   359 NITHVPGGGNKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 NITHVPGGGNKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418

Qy   419 MVDSPQLATLADEVSASLAKQGL 441
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Db   419 MVDSPQLATLADEVSASLAKQGL 441

RESULT   2
ORB0T1
microtubule-associated protein tau, form 1 - bovine
N;Contains: microtubule-associated protein tau, form 2
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A31939; A33914; S04005; A48885; A28173; B33734
R;Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
Mol. Cell. Biol. 9, 1381-1388, 1989
A;Title: Tau consists of a set of proteins with repeated C-terminal microtubule-bindi
A;Reference number: A31939; MUID:89261765
A;Accession: A31939
A;Molecule type: mRNA
A;Residues: 1-448 <HIM>
R;Iqbal, K.; Grundke-Iqbal, I.; Smith, A.J.; George, L.; Tung, Y.C.; Zaidi, T.
A;Experimental source: brain
A;Cross-references: GB:M26157; NID:g514913; PIDN:AAA30770.1; PID:g514914
Proc. Natl. Acad. Sci. U.S.A. 86, 5646-5650, 1989
R;Iqbal, K.; Smith, A.J.; Zaidi, T.; Grundke-Iqbal, I.
FEBS Lett. 248, 87-91, 1989
A;Title: Microtubule-associated protein tau. Identification of a novel peptide from b
A;Reference number: S04005; MUID:89252057
A;Accession: S04005
A;Molecule type: protein
A;Residues: 28/'A',30-38, IG',41,'AP',44,'LK' <IQ2>
A;Experimental source: brain
A;Note: 40-Pro was also found
R;Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
J. Biol. Chem. 268, 23512-23518, 1993
A;Title: Brain proline-directed protein kinase phosphorylates tau on sites that are a
A;Reference number: A48885; MUID:94043150
A;Accession: A48885
A;Molecule type: protein
A;Residues: 'X',203-208,'X',210-211,'X',213-216;238-241,'X',243-247,'X',404-410,'X',4
A;Experimental source: brain
A;Note: sequence modified after extraction from NCBI backbone
R;Aizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
J. Biol. Chem. 263, 7703-7707, 1988
A;Title: Microtubule-binding domain of Tau proteins.
A;Reference number: A28173; MUID:88227970
A;Accession: A28173
A;Molecule type: protein
A;Residues: 205-218,'X',220-223 <AIZ>
A;Experimental source: brain
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
F;1-448/Product: microtubule-associated protein tau, form 1 #status predicted <BT4>
F;1-174,193-448/Product: microtubule binding #status experimental
F;205-223/Region: microtubule binding #status experimental
F;259-289/Domain: MAP2/tau repeat homology <MT1>
F;290-320/Domain: MAP2/tau repeat homology <MT2>
F;321-351/Domain: MAP2/tau repeat homology <MT3>
F;352-383/Domain: MAP2/tau repeat homology <MT4>
F;202,209,242,248,411/Binding site: phosphate (Ser) (covalent) (by proline-directed k
F;212/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status e

Query Match   87.6%;   Score 2011.5;   DB 1;   Length 448;

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Best Local Similarity 86.7%; Conservative 9; Pred. No. 2.2e-96; Mismatches 21; Indels 31; Gaps 4;
Matches 399;

Qy    1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMH-QEGDTDAGLKESPLQTPTEDGSEEP 59
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Db    1 MAEPRQEFDVMEDHA--------QGDTYLQDQOEGDMDPGLIKESPLQTPADDGSEEP 48

Qy   60 GSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAA 119
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Db   49 GSETSDAKSTPTAEDATAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTSNLEDQAA 108

Qy  120 GHVTQARMVSKSKDGTGSDDKKAKGADGK--TKIATPRGAAPPGQKGQANATRIPAKTPP 177
          ||||||||||| ||||| |||| |||||   ||||||||||||||||||||||||||| |
Db  109 GHVTQARMVSKGKDGTGPDDKKTKGADGKPGTKIATPRGAAPPGQKGQANATRIPAKTTP 168

Qy  178 APKTPPSS---------------GEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTR 221
          :||| ::              :|||||||||||||||||||||||||||||||||||||
Db  169 TPKTSPATMVQKKPPPAGAKSERGESGKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTR 228

Qy  222 EPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKK 281
          |||||||||||||||||:||||||:||:|||||||||||||||||||||||||||||||||
Db  229 EPKKVAVVRTPPKSPSSAAKSRLQAAPGPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKK 288

Qy  282 LDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKS 341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  289 LDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKS 348

Qy  342 EKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSG 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  349 EKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSG 408

Qy  402 DTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL 441
          ||||||||||||||||||||||||||||||||||||||||
Db  409 DTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL 448
```

```
RESULT  3
JS0306
microtubule-associated protein tau - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993
C;Accession: JS0306; A33574
A;Note: the sequence shown is from adult rat brain
A;Note: the partial sequence from fetal rat brain is lacking residues 266-296; the fetal
A;Note: both fetal and adult forms were found in the paired helical filaments characteri
R;Kanai, Y.; Takemura, R.; Oshima, T.; Mori, H.; Ihara, Y.; Yanagisawa, M.; Masaki, T.;
J;Cell Biol. 109, 1173-1184, 1989
A;Title: Expression of multiple tau isoforms and microtubule bundle formation in fibrobl
A;Reference number: A33574; MUID:8935909
A;Accession: A33574
A;Molecule type: mRNA
A;Residues: 1-432 <KAN>
A;Note: a variant lacking residues 63-91 was also found
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; Alzheimer's disease; calmodulin binding; microtubule b
F;243-273/Domain: MAP2/tau repeat homology <MT1>
F;274-304/Domain: MAP2/tau repeat homology <MT2>
F;305-335/Domain: MAP2/tau repeat homology <MT3>
F;336-367/Domain: MAP2/tau repeat homology <MT4>
F;282-313/Disulfide bonds: #status experimental
F;347/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match          87.3%;  Score 2003.5;  DB 2;  Length 432;
Best Local Similarity 88.1%;  Pred. No. 5.3e-96;
```

```
Matches 392; Conservative 15; Mismatches 21; Indels 17; Gaps 3;

Qy    1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMH--HQEGDTDAGLKESPPQPADDGSEE 58
          |||||||| ||||  :           |||| |    |||||| ||||||| || |||||
Db    1 MAEPRQEFDVMEDQAGD-----------YTMLQDQOEGDMDHGLIKESPPQPADDGSEE 47

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
          |||||||||||||||||||||| :|||:||| ||| |||||||||||||||||||  |  
Db   48 PGSETSDAKSTPTAEDVTAPLVEERAPDKQATAQSHEIPEGTTAEEAGIGDTPNMEDQA 107

Qy  119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKI--KIATPRGAAPPGQKGQANATRIPAKTP 176
          ||||||| ||| :||:    |||||| ||    ||||||||||||:||||||||||||| 
Db  108 AGHVTQARVAGVSKDRIGNDEKKAKGADGKTGAKIATPRGAAPPGQKGTSNATRIPAKTT 167

Qy  177 PAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 236
          ||||| |::|:||||||||||||||||||||||||||||||||||||||||||||||||||
Db  168 PSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 227

Qy  237 SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 296
          ||:||||||:||:||||||||||||||||||||||||||||||||||||||||||||||||
Db  228 SASKSRLQAAPGPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 287

Qy  297 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 356
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  288 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 347

Qy  357 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  348 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 407

Qy  417 IDMVDSPQLATLADEVSASLAKQGL 441
          |||||||||||||||||||||||||
Db  408 IDMVDSPQLATLADEVSASLAKQGL 432
```

```
RESULT  4
A38235
microtubule-associated protein, 110K tau - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999
C;Accession: A38235
A;cross-references: GB:M84156; NID:g207157; PIDN:g207157; PIDN:AAA42204.1; PID:g207158
A;Note: sequence extracted from NCBI backbone (NCBIN:87258, NCBIP:87359)
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; tandem repeat
R;Goedert, M.; Spillantini, M.G.; Crowther, R.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1983-1987, 1992
A;Title: Cloning of a big tau microtubule-associated protein characteristic of the pe
A;Reference number: A38235; MUID:92179305
A;Accession: A38235
A;Molecule type: mRNA
A;Residues: 1-686 <GOE>

Query Match          81.1%;  Score 1861.5;  DB 2;  Length 686;
Best Local Similarity 55.9%;  Pred. No. 1.6e-88;
Matches 391; Conservative 15; Mismatches 22; Indels 271; Gaps 4;

Qy    1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTM--HQEGDTDAGLKESPLQTPTEDGSEE 58
          |||||||| |||: |           |||| |    |||||| ||||||| || ||||||
Db    1 MAEPRQEFEDVMEDQAGD-----------YTMLQDQOEGDMDHGLIKESPPQPADDGSEE 47

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
          |||||||||||||||||||||| :|||:||| ||| |||||||||||||||||||  |  
Db   48 PGSETSDAKSTPTAEDVTAPLVEERAPDKQATAQSHEIPEGTTAEEAGIGDTPNMEDQA 107

Qy  119 AGHVTQ---------- 124
          ||||||
Db  108 AGHVTQEPQKVEIFSQSLLVEPGRREGQOAPDSGISDWTHQQVPSMSGAPLPPQGLREATH 167
```

RESULT 5

```
Qy   125  ------------------------------------------------------------  124

Db   168  QPLGTPPEDVERSHPASELLWQESPQKEAWGKDRLGSEEEVDEDITMDESSQESSPSQAS  227

Qy   125  ------------------------------------------------------------  124

Db   228  LAPGTATPQARSVSASGVGGEETTSIPGFPAEGSIPLPADFFSKVSAETQASPEGPGTGP  287

Qy   125  ------------------------------------------------------------  124

Db   288  SEEGHEAAPEFTHVEIKASAPKEQDLEGATVVGAPAEEQKARGPSVGKGTKEASLLEPT   347

Qy   125  ------------------------------------------------------------  124

Db   348  DKQPAAGLPGRPVSRVPQLKARVAGVSKDRTGNDEKKAKGADGKTGAKIATPRGAATPGQ  407

Qy   125  ------ARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQ                162
               |||:| |||||||||||||||||||||
Db   408  KGTSNATRIPAKTPSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTRE   467

Qy   163  KGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTRE  222
          |::|||||||| |:||||| |||||||||:||||||||||||||||||||||||||||||
Db   468  PKKVAVVRTPPKSPSASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKL  527

Qy   223  PKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKL  282
          ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db   528  DLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSE  587

Qy   283  DLSNVQSKCGSKDNIKHVPGGGSVQIVYKRVDLSKVTSKCGSLGNIHHKPGGGQVEVKSE  342
          |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db   588  KLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGD  647

Qy   343  KLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGD  402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   648  TSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL                       686

Qy   403  TSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL                       441
          ||||||||||||||||||||||||||||||||||||||
```

Query Match   79.3%;   Score 1821;   DB 2;   Length 733;

Best Local Similarity 52.4%;   Pred. No. 2.1e-86;
Matches 391;   Conservative 15;   Mismatches 22;   Indels 318;   Gaps 6;

RESULT 6

```
Qy     1  MAEPRQEFEVMEDHAGDQDTGLGDRKDQGGYTM--HQEGDTDAGLKESPLQTPTEDGSEE   58
          |||||||| |||||||                   |:  |||||||||:||||||||:||
Db     1  MANPRQEFNTMEDHAGD-------------------YTILDQDEGDMDHGLKESPQPPADDGAEE  47

Qy    59  PGSEISDAKSTPTAEDVTAPLVDEGAPGRQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA  118
          |||| ||||||||||||||||||||:|||:|||||||||||||||:|||||||||::|||
Db    48  PGSETSDAKSTPTAEDVTAPLVDERAPDKQAAAQPHTEIPEGITAEEAGIGDTPNQEDQA  107

Qy   119  AGHVTQARM---------------------------------------------------  127
          |||||||:|
Db   108  AGHVTQGRREGQAPDLGTSDWTRQQVSMSGAPLLPQGLREATCQPSGTRPEDIEKSHPA   167

Qy   128  ------------------------------------------------------------  127

Db   168  SELLRRGPGPQKEGWGQDRLGSEEEVDEDITVDESSQDSPPSQASLTPGRAAPQAGSGSYC  227

Qy   128  ------------------------------------------------------------  127

Db   228  GETASVPGLPTEGSVPLPADFFSKVSAETQASQEPGPGTGPMEEGHEAAPEFTHVEIKA   287

Qy   128  ------------------------------------------------------------  127

Db   288  STPKEQDLEGATVVGVPGPEEQKAQTQGPSVGKGTKEASLQEPPGKQPAAGLPGRPVSRVP  347

Qy   131  SKDGTGSDDKRA------------------------------------------------  142
           |:|:|:||:|
Db   348  QLKARVASKDRTGNDEKKARTSTPSCARAPSHRPCLSPTRPTLGSSDPLIKPSSPAVSPE  407

Qy   143  ------KGADGKT--KIATPRGAAPPGQGKGQANATRIPAKT                    175
                ||||||  |||||||||:         ||||||||||
Db   408  PATSPKHVSSVTPRNGSPGTKQMLKGADGKTGAKIATPRGAASPAQKGTSNATRIPAKT   467

Qy   176  PPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKS  235
          ||:|||||:|||||||||:||||||||||||||||||||||||||||||||||||||||||
Db   468  TPSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKS  527

Qy   236  PSSAKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKD  295
          |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   528  PSASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKD  587

Qy   296  NIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIG  355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   588  NIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIG  647

Qy   356  SLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTG  415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   648  SLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTG  707

Qy   416  SIDMVDSPQLATLADEVSASLAKQGL                                    441
          ||||||||||||||||||||||||||
Db   708  SIDMVDSPQLATLADEVSASLAKQGL                                    733
```

```
F;216-246/Domain: MAP2/tau repeat homology <MT2>
F;247-277/Domain: MAP2/tau repeat homology <MT3>
F;278-309/Domain: MAP2/tau repeat homology <MT4>

Query Match             74.5%;  Score 1710.5;  DB 2;  Length 374;
Best Local Similarity   76.9%;  Pred. No. 4.6e-81;
Matches  342;  Conservative   14;  Mismatches   14;  Indels   75;  Gaps    4;

Qy    1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTM--HQEGDTDAGLKESPLQTPTEDGSEE 58
         ||||||||:|:|| ||:                  :|| |  ||| |:
Db    1 MAEPRQEFDTMEDQAGD-----------------YTMLQDQEGDMDHGLK---------- 33

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
                                                        |||||||| :|:|:
Db   34 ------------------------------------AEEAGIGDTPNMEDQA 49

Qy  119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQKGQANATRIPAKTP 176
         ||||||||  ::::| :|::|:|:||||||| | ||||||| ||||||: :|||||||:
Db   50 AGHVTQARVAGVSKDRTGNDEKRAKGADGKTGAKIATPRGAAPPGQKGTSNATRIPAKTT 109

Qy  177 PAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 236
         | ||||  ||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db  110 PSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 169

Qy  237 SSAKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 296
         |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  170 SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 229

Qy  297 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 356
         ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db  230 IKHVPGGGSVQIYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 289

Qy  357 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416
         |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db  290 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVHKSPVVSGDTSPRHLSNVSSTGS 349

Qy  417 IDMVDSPQLATLADEVSASLAKQGL 441
         |||||||||||||||||||||||||
Db  350 IDMVDSPQLATLADEVSASLAKQGL 374

RESULT  7
QRHUT2
microtubule-associated protein tau, fetal (clone p18) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 02-Sep-1997
C;Accession: PN0001
R;Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A;Title: The microtubule binding domain of tau protein.
A;Reference number: JN0009; MUID:90180482
A;Accession: PN0001
A;Molecule type: mRNA
A;Residues: 1-316 <LEE>
A;Genetics:
C;Gene: GDB:119434; OMIM:157140
A;Gene: GDB:MAPT; MTBT1
C;Map position: 17q21-17q21
A;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule binding;
A;Note: this sequence differs from a previously reported fetal tau protein sequence only
F;158-188/Domain: MAP2/tau repeat homology <MT1>
F;189-219/Domain: MAP2/tau repeat homology <MT2>
F;220-251/Domain: MAP2/tau repeat homology <MT3>

Query Match             67.9%;  Score 1558.5;  DB 1;  Length 316;
Best Local Similarity   90.8%;  Pred. No. 2.3e-73;
Matches  306;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy  105 EAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKG 164
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11 EAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIAIPRGAAPPGQKG 70

Qy  165 QANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPK 224
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   71 QANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPK 130

Qy  225 KVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDL 284
         ||||||||||||:|||||||||||||||||||||||||||||||||||||
Db  131 KVAVVRTPPKSPSASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGK---------- 180

Qy  285 SNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKL 344
                              ||:|||||||||||||||||||||||||||||||||||||||
Db  181 ------------------------VQIYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKL 219

Qy  345 DFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTS 404
         |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db  220 DFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVHKSPVVSGDTS 279

Qy  405 PRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL 441
         |||||||||||||||||||||||||||||||||||||
Db  280 PRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL 316

RESULT  8
B28820
microtubule-associated protein tau type 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: B28820
R;Lee, G.; Cowan, N.; Kirschner, M.
Science 239, 285-288, 1988
A;Title: The primary structure and heterogeneity of tau protein from mouse brain.
A;Reference number: A94298; MUID:88099510
A;Accession: B28820
A;Molecule type: mRNA
A;Residues: 1-341 <LEE>
C;Cross-references: GB:M18775; NID:g201114; PIDN:AAA40165.1; PID:g201115
A;Cross-references: GB:M18775; NID:g201114; PIDN:AAA401165.1; PID:g201115
A;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; tandem repeat
F;183-213/Domain: MAP2/tau repeat homology <MT1>
F;214-244/Domain: MAP2/tau repeat homology <MT2>
F;245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match             65.9%;  Score 1512;  DB 2;  Length 341;
Best Local Similarity   69.7%;  Pred. No. 6e-71;
Matches  310;  Conservative   14;  Mismatches   13;  Indels  108;  Gaps    6;

Qy    1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTM--HQEGDTDAGLKESPLQTPTEDGSEE 58
         ||:|||||:||||:||:                  :||  |  ||| |:
Db    1 MADPRQEFDTMEDHAGD-----------------YTLLQDQEGDMDHGLK---------- 33

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
                                                        |||||||| :|:|:
Db   34 ------------------------------------AEEAGIGDTPNQEDQA 49

Qy  119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAASPAQKGQANATRIPAKTP 176
         ||||||||  ::::| :|::|:|:||||||| | ||||||| :| |||: :|||||||:
Db   50 AGHVTQARVA--SKDRTGNDEKRAKGADGKTGAKIATPRGAAPPGQKGTSNATRIPAKTT 107

Qy  177 PAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 236
         | ||||  ||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db  108 PSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 167

Qy  237 SSAKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 296
         |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  168 SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 227

Qy  297 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 356
               ||:|||||||||||||||||||||||||||||||||||||
Db  206 ------VQIYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 256

Qy  357 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416
```

```
Db  257  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  417  IDMVDSPQLATLADEVSASLAKQGL 441
         |||||||||||||||||||||||||
Db  317  IDMVDSPQLATLADEVSASLAKQGL 341
```

RESULT 9

A28820

microtubule-associated protein tau type 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: A28820
R;Lee, G.; Cowan, N.; Kirschner, M.
Science 239, 285-288, 1988
A;Title: The primary structure and heterogeneity of tau protein from mouse brain.
A;Reference number: A94298; MUID:88099510
A;Accession: A28820
A;Molecule type: mRNA
A;Residues: 1-364 <LEE>
A;Cross-references: GB:M18776; NID:g201116; PIDN:AAA40166.1; PID:g201117
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; tandem repeat
F;183-213/Domain: MAP2/tau repeat homology <MT1>
F;214-244/Domain: MAP2/tau repeat homology <MT2>
F;245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match   65.7%; Score 1508; DB 2; Length 364;
Best Local Similarity   69.6%; Pred. No. 1e-70;
Matches 309; Conservative 14; Mismatches 13; Indels 108; Gaps 6;

```
Qy    1  MAEPRQEFEVMEDHAGDTYGLGDRKDQGGYTM--HQEGDTDAGLKESPLQTPTEDGSEE 58
         |||||||||||||||||||||||||||||||  |: |::||||||||||||||||||||
Db    1  MADPRQEFDTMEDHAGD-----YTLLQDQEGDMDHGLK------------------- 33

Qy   59  PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
         |||:||||||||||||||||||||||||||||||||:|||||:||||||||||||||:|:
Db   34  -------------------------------------AEEAGIGDTPNQEDQA 49

Qy  119  AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQKGQANATRIPAKTP 176
         |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db   50  AGHVTQARVA--SKDRTGNDEKKAKGADGKTGAKIAIPRGAASPAQKGTSNATRIPAKTT 107

Qy  177  PAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 236
         ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  108  PSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 167

Qy  237  SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 296
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  168  SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGK------------------- 205

Qy  297  IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 356
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db  206  ------VQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 256

Qy  357  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  257  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 316

Qy  417  IDMVDSPQLATLADEVSASLAKQG 440
         ||||||||||||||||||||||||
Db  317  IDMVDSPQLATLADEVSASLAKQG 340
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RESULT 10

QRBOT2

microtubule-associated protein tau, form 3 - bovine
N;Contains: microtubule-associated protein tau, form 4; microtubule-associated protein tau, form 4; microtubule-associated protein t
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 31-Mar-1996
C;Accession: B31939; A48885; A28173

R;Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
Mol. Cell. Biol. 9, 1381-1388, 1989
J. Biol. Chem. 268, 23512-23518, 1993
A;Title: Brain proline-directed protein kinase phosphorylates tau on sites that are a
A;Reference number: A48885; MUID:89261765
A;Accession: A48885
A;Molecule type: protein
A;Residues: 1-402 <HIM>
A;Cross-references: GB:M26157; GB:M26158
R;Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
J. Biol. Chem. 268, 23512-23518, 1993
A;Title: Tau consists of a set of proteins with repeated C-terminal microtubule-bindi
A;Reference number: A31939; MUID:89261765
A;Accession: B31939
A;Molecule type: protein
A;Residues: 'X',157-162,'X',164-165,'X',167-170:192-195,'X',197-201,'X',358-364,'X',3
A;Note: sequence modified after extraction from NCBI backbone
R;Aizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
J. Biol. Chem. 263, 7703-7707, 1988
A;Title: Microtubule-binding domain of Tau proteins.
A;Reference number: A28173; MUID:88227970
A;Accession: A28173
A;Molecule type: protein
A;Residues: 159-172,'X',174-177 <AIZ>
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Experimental source: brain
C;Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
F;1-234:297-402/Product: microtubule-associated protein tau, form 4 #status predicted
F;101-402/Product: microtubule-associated protein tau, form 4 #status predicted <BT5>
F;101-402/Region: microtubule binding #status experimental
F;159-177/Domain: MAP2/tau repeat homology <MT1>
F;213-243/Domain: MAP2/tau repeat homology <MT2>
F;244-274/Domain: MAP2/tau repeat homology <MT3>
F;275-305/Domain: MAP2/tau repeat homology <MT4>
F;306-337/Domain: MAP2/tau repeat homology
F;156,163,196,202,365/Binding site: phosphate (Ser) (covalent) (by proline-directed k
F;166/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status F

Query Match   65.1%; Score 1493; DB 1; Length 402;
Best Local Similarity   79.7%; Pred. No. 6.7e-70;
Matches 303; Conservative 14; Mismatches 29; Indels 34; Gaps 6;

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Qy   64  SDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVT 123
         |||::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   55  SPKRPTPGSSD---PLIKPSSD--------------AVCPEPSSSPK----------- 87

Qy  124  QARMVSKSKDGTGSDDKKAKGADGK--TKIATPRGAAPPGQKGQANATRIPAKTPPAPKT 181
         :|| |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db   88  S---VIPRTGNSGAKEMKVRGADGKPGTKIATPRGAAPPGQKGQANATRIPAKTTPSPKT 144

Qy  182  PPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAKS 241
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|:||
Db  145  SP--GESGSKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSAAKS 202

Qy  242  RLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVP 301
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  203  RLQAAPGPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVP 262

Qy  302  GGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNIT 361
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  263  GGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNIT 322

Qy  362  HVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVD 421
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  323  HVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVD 382

Qy  422  SPQLATLADEVSASLAKQGL 441
         ||||||||||||||||||||
Db  383  SPQLATLADEVSASLAKQGL 402
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RESULT 11

I67793
microtubule-associated protein 2, splice form MAP-2c - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Dec-1998
A;Accession: I67793
R;Albala, J.S.; Kalcheva, N.; Shafit-Zagardo, B.
Gene 136, 377-378, 1993
A;Reference number: I67793
A;Title: Characterization of the transcripts encoding two isoforms of human microtubule-
A;Cross-references: GB:L12563; NID:g348216; PID:g348217
A;Accession: I67793
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-472 <ALB>
A;Cross-references: GB:L12563; NID:g348216; PID:g348217
C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
A;Gene: GDB:MAP2; MAP2A; MAP2B; MAP2C
C;Genetics:
A;Residues: 1-472 <ALB>
A;Cross-references: GDB:118836; OMIM:157130
A;Map position: 2q34-2q34
A;Introns: 151/3
F;314-344/Domain: MAP2/tau repeat homology <MT1>
F;376-407/Domain: MAP2/tau repeat homology <MT3>

Query Match   32.5%;   Score 746.5;   DB 2;   Length 472;
Best Local Similarity   37.6%;   Pred. No. 1.3e-31;
Matches   184;   Conservative   60;   Mismatches   126;   Indels   119;   Gaps   12;

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Qy     8  FEVMEDHAGQDTYGLGDRKDQGGYTMHQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAK   67
          |::      :||| |   | |  ||
Db    48  FPYREDEEG----AFGEHGSOGTYSNTKENGINGELTSADRETAEEVSARIVQVVTAEAV  103

Qy    68  STPTAE-------DVTA--PLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDT----PSL  114
          : ||         ||||   |  |  |          |   :||||||||       |
Db   104  AVLKGEQEKEAQHKDQTAJLPLAAAEETANLPPSPPPSPASEQTVVEEAAGGESALAPSV  163

Qy   115  EDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPP--------------  160
          |||||||||||||||||||||||||||||||||||||||||||||
Db   164  FKQAKDKVS-----------DGVTKSPEKRSSLPRPSSILPPRGVSGDRDENSFS       208

Qy   161  ------------GQKQOANARIPAKTPPAPKTPPSSGEPPKSGDRSGYSS            199
                       || |  ||  |||||||||||| ||||||||||||
Db   209  LNSSISSAARTTRSEPIRRAGKSGNTSPTPT-TPGSTAITPGTPPS--------YSS     255

Qy   200  --PGSSPGTPGSSRKPSLPIPP--------TREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPD  252
            |||| ||| | |  |  |          ||| ||||||||||| ||| ||
Db   256  RTPGTPGTP-SYPRPHTPGTPKSAILVPSEKKVAIIRTPPKSPGLTPKQLRLINQPLPD     314

Qy   253  LKNVKSKIGSTENLKHOPGGGKVQINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIYKP      312
          ||||||||||| |: | |||| |||| ||||||||| ||||||||| |||||||| |
Db   315  LKNVKSKIGSTDNIKYQPKGGQVQIVTKIDLSH------------------------      348
```

R;Kindler, S.; Schulz, B.; Goedert, M.; Garner, C.C.
J. Biol. Chem. 265, 19679-19684, 1990
A;Title: Molecular structure of microtubule-associated protein 2b and 2c from rat bra
A;Reference number: A37981
A;Accession: A37981
A;Molecule type: mRNA
A;Residues: 1-1830 <KIN>
A;Cross-references: GB:X51842; NID:g56620; PIDN:CAA36135.1; PID:g56621
A;Accession: B37981
A;Molecule type: mRNA
A;Residues: 1-151,1515-1830 <KI3>
A;Accession: S10003
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-830 <KI2>
A;Accession: S07887
A;Cross-references: EMBL:X51842; NID:g56620; PIDN:CAA36135.1; PID:g56621
R;Doll, T.; Papandrikopoulou, A.; Matus, A.
Nucleic Acids Res. 18, 361, 1990
A;Title: Complete cDNA sequence encoding rat high and low molecular weight MAP2.
A;Reference number: S10003; MUID:90251471
A;Accession: S10003
A;Molecule type: mRNA
A;Residues: 1-476, 'H', 478-486, 'E', 488-525, 'R', 527-665, 'V', 667-670, 'R', 672-872, 'R', 874
A;Cross-references: EMBL:X53455; NID:g57619; PIDN:CAA37535.1; PID:g57620
C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
A;Gene: map2
C;Genetics:
A;Accession: S07887; MUID:90221819
A;Molecule type: mRNA
A;Residues: 1-151,1515-1830 <DOL>
A;Cross-references: EMBL:X17682; NID:g56622; PIDN:CAA35667.1; PID:g56623
R;Matus, A.; Doll, T.
submitted to the EMBL Data Library, May 1990
A;Reference number: S14568
A;Accession: S14568
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-476 <H'>
A;Cross-references: EMBL:X53455; NID:g57619; PIDN:CAA37535.1; PID:g57620
C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; tandem repeat
F;1-1830/Product: microtubule-associated protein 2b #status predicted <M2B>
F;1-151,1515-1830/Product: MAP2/tau repeat homology <MT1>
F;1672-1702/Domain: MAP2/tau repeat homology <MT2>
F;1703-1733/Domain: MAP2/tau repeat homology <MT3>
F;1734-1765/Domain: MAP2/tau repeat homology <MT3>

Query Match   31.5%;   Score 723;   DB 2;   Length 1830;
Best Local Similarity   39.4%;   Pred. No. 9e-30;
Matches   176;   Conservative   64;   Mismatches   109;   Indels   98;   Gaps   13;

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Qy    44  KESPLQT------------PTEDGSEEPGSETSDAKSPTAEDVTAPLVDEG           89
          ||| |:              ||||||||||||:|||||| || |: |
Db  1433  KEKPFKTGRGRISTEPRREVAKKEPSTVSRDEVRRKKAVYKKAELAKESEVQAHSFSRKL  1492

Qy    90  AAQPHTE----------IPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDDK  140
          | |||||          |||||||||||||  |||||||||||||||||||||||||
Db  1493  ILKPAIKYTRPTHLSCVKRKITATSGGESAQPSAFKQAKDKVT--------------DG   1537

Qy   141  KAKGADGKTKIATPRGAAPP---GQKG--QANATRIPAKTPPAPKTPPSSGEPPKSGDRSG  196
          |||||||||||||||||||    | |   |||| |||||||||||||||||||||
Db  1538  ITKSPEKRSSLPRPSSILPPRRGVSGDRDENSFSLNSSISSAARTTRS-EPIRRAGKSG   1595

Qy   197  YSSPGSPG---------TPGS-----RSRTPSLPTPPT--REP----------KKVAVVRTPPK  234
          ||| ||           |||      || ||| | |     |            |||||||||
Db  1596  TSTPTPGSTAITPGTPPPSYSSRTPGTPGTPSYPRPHTPGTPKSGILVPSEKKVAIIRTPPK  1655

Qy   235  SPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHOPGGGKVQINKKLDLSNVQSKCGSK      294
          |||| ||||| |  | |||||||||||| |: | |||| |||| ||||||||| |||
Db  1656  SPATPK-QLRLINQPLPDLKNVKSKIGSTDNIKYQPKGGQVQIVTKIDLSH--------   1706

Qy   295  DNIKHVPGGGSVQIYKPVDLSKVTWSKCGSLGNIHHKPGGGQVEKSEKLDFKDRVQSKI    354
          |||||||||||  |      ||| |||||||||||||||| || ||||||||||||
Db          ...
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Db 1707 ---------------------VTSKCGSLKNIRHRPGGGVRKIESVKLDFKEKAQAKV 1743

Qy 355 GSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSST 414
    |||::|||||||||:||||:||||||||||::|||||||||||||| ||| |||:|||
Db 1744 GSLDNAHHVPGGGNVKIDSQKLNFREHAKARVDHGAEIITQSPSRSSVASPRRLSNVSSS 1803

Qy 415 GSIDMVDSPQLATLADEVSASLAKQGL 441
    ||:||||:|||||:||:||:|:|||||
Db 1804 GSINLLESPQLATLAEDVTAALAKQGL 1830

RESULT 13
A40115
microtubule-associated protein MAP2 - mouse
N;Alternate names: MAP2
C;Species: Mus musculus (house mouse)
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 13-Aug-1999
C;Accession: A40115; S06467
R;Lewis, S.A.; Wang, D.; Cowan, N.J.
Science 242, 936-939, 1988
A;Title: Microtubule-associated protein MAP2 shares a microtubule binding motif with tau
A;Reference number: S06467; MUID:89043973
A;Accession: A40115
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1828 <LEW>
A;Cross-references: GB:M21041; NID:g199022; PIDN:AAA39490.1; PID:g199023
R;Wang, D.; Lewis, S.A.; Cowan, N.J.
Nucleic Acids Res. 16, 11369-11370, 1988
A;Title: Complete sequence of a cDNA encoding mouse MAP2.
A;Reference number: S06467; MUID:89083571
A;Accession: S06467
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-1828 <WAN>
A;Cross-references: GB:M21041; NID:g199022; PIDN:AAA39490.1; PID:g199023
C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
C;Keywords: microtubule binding; tandem repeat
F;1670-1700/Domain: MAP2/tau repeat homology <MT1>
F;1701-1731/Domain: MAP2/tau repeat homology <MT2>
F;1732-1763/Domain: MAP2/tau repeat homology <MT3>

Query Match 31.4%; Score 719.5; DB 2; Length 1828;
Best Local Similarity 39.6%; Pred. No. 1.4e-29;
Matches 176; Conservative 61; Mismatches 113; Indels 95; Gaps 13;

Qy 44 KESPLQT-----------PTEDGSEEPGGSETSDAKSTPTAEDVTAPL-----VDEGAPGKQAA 90

Db 1432 KEKPFKTGRGRISTPERKVAKKEPSTVSRDEVRRKAVYKKAELAKKSEVQAHSPSRKLI 1491

Qy 91 AQPHTE-----------IPEGTTAEEAGIGDIPSLEDEAAGHVTQARMVSKSKDGTG---- 136

Db 1492 LKPAIKYTRPTHLSCVRKRTTAASGDLAQAPGAFKQAKDKVTDG----ISKSPEKRSSLPRP 1549

Qy 137 --------SDDKRAKGADGKTKIATPRGAA----------PPGQKGQANATRIPAKTPPAPK 180

Db 1550 SSILPPRGVSGDREENSFSLNSSISSARRTTRSEPIRRAGKSGTSTPT-TPGSTAITPG 1608

Qy 181 TPPSSGEPPKSGDRSGYSS----PGSPGTPGSRSRTPSLPTPPTREP--KKYAVVRTPPKSP 236

Db 1609 TPPS--------------------YSRRTPGTPGTP-SYPRTPTPKGGILVPSEKKVAIRTPPKSP 1655

Qy 237 SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQOIINKKLDLSNVQSKCGSKDN 296

Db 1656 ATPK-QLRLINQPLPDLKNVKSKIGSTDNIKYQPRGGQVQIVTKKIDLSH------------ 1704

Qy 297 IKHVPGGGVQIVYKPVDLSKVTSKCGSLGNIHKRPGGGGQVEVKSEKLDFKDRVQSKIGS 356

Db 1705 ---------------------VTSKCGSLKNIRHRPGGGRVKIESVKLDFKEKAQAKVGS 1743

Qy 357 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416

Db 1744 LDNAHHVPGGGNVKIDSQKLNFREHAKARVDHGAEIITQSPSRSSVASPRRLSNVSSSGS 1803

Qy 417 IDMVDSPQLATLADEVSASLAKQGL 441

Db 1804 INLLESPQLATLAEDVTAALAKQGL 1828

RESULT 14
S13507
microtubule-associated protein MAP2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C;Accession: S13507
R;Marechal, D.; Delaplerre, D.; Dresse, A.
Arch. Int. Physiol. Biochim. 96, 231-236, 1988
A;Title: Cloning and partial sequencing of a new rat brain specific cDNA.
A;Reference number: S13507; MUID:89334524
A;Accession: S13507
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-1825 <MAR>
A;Cross-references: EMBL:X54100; NID:g56624; PIDN:CAA38034.1; PID:g56625
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1990
C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
C;Keywords: microtubule binding; tandem repeat
F;1667-1697/Domain: MAP2/tau repeat homology <MT1>
F;1698-1728/Domain: MAP2/tau repeat homology <MT2>
F;1729-1760/Domain: MAP2/tau repeat homology <MT3>

Query Match 31.3%; Score 717.5; DB 2; Length 1825;
Best Local Similarity 39.2%; Pred. No. 1.7e-29;
Matches 175; Conservative 65; Mismatches 109; Indels 97; Gaps 13;

Qy 44 KESPLQT-----------PTEDGSEEPGGSETSDAKSTPTAEDVTAPL-----VDEGAPGKQAA 90

Db 1429 KEKPFKTGRGRISTPERKVAKKEPSTVSRDEVRRKAVYKKAELAKKSEVQAHSPSRKLI 1488

Qy 91 AQPHTE-----------IPEGTTAEEAGIGDIPSLEDEAAGHVTQARMVSKSKDGTGSDDKK 141

Db 1489 LKPAIKYTRPTHLSCVRKRTTATSGESAQAPSAFKQAKDKVT--------------------DGI 1533

Qy 142 AKGADGKTKIATPRGAAPP--GQKG--QANATRIPAKTPPAPKTPPSSGEPPKSGDRSGY 197

Db 1534 TKSPEKRSSLPRPSSILPPRRGVSGDREENSFSLNSSISSARRTTRS--EPIRRAGKSGT 1591

Qy 198 SSPGSPG----TPGS---RSRTPSLPTPPT--REP------------KKYAVVRTPPKS 235

Db 1592 STPTTPGSTAITPGTPSYSSRTPGTPGTPSYPRTPTPKFGILVPSEKKVAIRTPPKS 1651

Qy 236 PSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQOIINKKLDLSNVQSKCGSKD 295

Db 1652 PATPK-QLRLINQPLPDLKNVKSKIGSTDNIKYQPRGGQVQIVTKKIDLSH---------- 1701

Qy 296 NIKHVPGGGSVQOIVYKPVDLSKVTSKCGSLGNIHKRPGGGGQVEVKSEKLDFKDRVQSKIG 355

Db 1702 -------------------VTSKCGSLKNIRHRPGGGRVKIESVKLDFKEKAQAKVG 1739

Qy 356 SLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTG 415

Db 1740 SLDNAHHVPGGGNVKIDSQKLNFREHAKARVDHGAEIITQSPSRSSVASPRRLSNVSSSG 1799

Qy 416 SIDMVDSPQLATLADEVSASLAKQGL 441

Db 1800 SINLLESPQLATLAEDVTAALAKQGL 1825

RESULT 15
QRHUMT
microtubule-associated protein 2, splice form MAP-2b - human
N;Alternate names: MAP2
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 12-Apr-1996 #text_change 22-Jun-1999

C;Accession: I53693; A61085; PL0024; S34131
R;Albala, J.S.; Kalcheva, N.; Shafit-Zagardo, B.
Gene 136, 377-378, 1993
A;Title: Characterization of the transcripts encoding two isoforms of human microtubule-
A;Reference number: I53693; MUID:94124038
A;Accession: I53693
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1824 <ALB>
A;Cross-references: EMBL:Z21958; GB:L12563; NID:g348201; PID:g348218
J;Dammerman, M.; Yen, S.H.; Shafit-Zagardo, B.
J. Neurosci. Res. 24, 487-495, 1989
A;Title: Sequence of a human MAP-2 region sharing epitopes with Alzheimer neurofibrillar
A;Reference number: A61085; MUID:90096190
A;Accession: A61085
A;Molecule type: mRNA
A;Residues: 489-1558 <KOS>
A;Cross-references: GB:M25668; NID:g187380; PIDN:AAA59552.1; PID:g187381
R;Kosik, K.S.; Orechio, L.D.; Bakalis, S.; Duffy, L.; Neve, R.L.
J. Neurochem. 51, 587-598, 1988
A;Title: Partial sequence of MAP2 in the region of a shared epitope with Alzheimer neuro
A;Reference number: PL0024; MUID:88274407
A;Accession: PL0024
A;Molecule type: mRNA
A;Residues: 77-645 <DAM>
A;Status: not compared with conceptual translation
A;Comment: Microtubule-associated proteins are a complex group consisting of the high mo
they may stabilize the microtubules against depolymerization.
C;Genetics:
A;Gene: GDB:MAP2
A;Cross-references: GDB:118836; OMIM:157130
A;Map position: 2q34-2q35
C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
F;1455-1463/Region: microtubule binding #status predicted
F;1666-1696/Domain: MAP2/tau repeat homology <MT1>
F;1697-1727/Domain: MAP2/tau repeat homology <MT2>
F;1728-1759/Domain: MAP2/tau repeat homology <MT3>
F;657,958,1064,1250,1436,1503/Binding site: phosphate (Thr) (covalent) #status predicted
F;697,817,829,1320,1417,1542,1551/Binding site: phosphate (Ser) (covalent) #status pred

Query Match   31.1%;   Score 713.5; DB 1;   Length 1824;
Best Local Similarity   36.5%;   Pred. No. 2.7e-29;
Matches 189;   Conservative 73;   Mismatches 137;   Indels 119;   Gaps 18;

Qy   2 AEPRQEEFEYMEDHAGQDTYGLGDRKDQ----GGYTMHQEG-------DTDAGLKESPLQT-P 51
             :| :|| | ||| ||:| | |||:| |: ||:: | ||| |
Db   1348 ASPERE-EVALSEYKTETY--DDYKDETTIDDSIMDADSLWVDTQDDDRSIMTEQLETIP 1404

Qy   52 TEDGSEEPGSETSDAK-----------------STP-----TAEDVTAPLVDE-----GAPGKQA   89
               ::|:|: | :|: ||| ||:   :|
Db   1405 KEEKAEKEARRSLEKHRKEKPFKTGRGRISTPERKVARKEPSTVSRDEVRRKAVYKKA 1464

Qy   90 AAQPHEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGS-------DDKKAK 143
             |: |: ||:| || | ::
Db   1465 ELAKKTEVQAHSPSRKFIL--KPAIKYTRPTHLSCVRKRTTAAGGESALAPSVFKQAKDK 1522

Qy   144 GADGKTKIATPRGAAP-------PGQKG------------------QANATRIPAKTP----- 176
             | || | |:| |:||: |: ||||||
Db   1523 VSDGVTKSPEKRSSLPRPSSILPPRGVSGDRDENSFSLNSSISSSAARTTRSEPIRRAG 1582

Qy   177 ---PAPKPPSS----GEPPKSGDRSGYSSSPGGSSPGTPGSRSRSPSLSTPPP-------TREP 223
               |:| |::| |::||:|| ||:| |:| : |:|:|:: ||
Db   1583 RSGTSPTPTPGSTAITPGTPPSYSSR-----TPGTPGT-SYRPTHPTGTPKSAILVPSE 1637

Qy   224 KKVAVRTPPKFSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGKVQIINKKLD 283
             | |:| || || ||:| |||:| :|||:| :|| | ||:| ||:::|| |
Db   1638 KRVAIIRTPPKSPGLTPKQLRLINQPLPDLKNVKSKIGSTDNIKYQPGGGQVQIVTKKID 1697

Qy   284 LSNVQSKGGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHKPGGGGQVEVKSEK 343
             |: :| ||||:|||:||||| ||::|| |||:|::|| ||| || |||| |||:||:|
Db   1698 LSH------VTSKCGSLKNIRHRPGGGRVKIESVK 1726

Qy   344 LDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKIDHGAEIVYKSPVVSGDT 403
             ||| |:: :|:||||| |||||| ||: | || |||| :||||||:|: |: | |
Db   1727 LDFKEKAQAKVGSLDNAHHVPGGGNVKIDSQKLNFREHAKARVDHGAEIITQSPGRSSVA 1786

Qy   404 SPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL 441
             |||| ||||| ||||:|||| |||:|::||::||||||
Db   1787 SPRRLSNVSSGGSINLLESPQLATLAEDVTAALAKQGL 1824

Search completed: September 28, 2000, 20:00:11
Job time: 3721 sec

OM protein - protein search, using sw model

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Run on: September 28, 2000, 19:59:12 ; Search time 47.83 Seconds
               (without alignments)
               285.724 Million cell updates/sec

Title: US-09-142-613-1
Perfect score: 2295
Sequence: 1 MAEPRQEFEVMEDHAGDTY..........SPQLATLADEVSASLAKQGL 441

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2262	98.6	441	1	TAU_HUMAN	P10636 homo sapien
2	2011.5	87.6	448	1	TAU1_BOVIN	P29172 bos taurus
3	2003.5	87.3	432	1	TAU1_RAT	P19332 rattus norv
4	1512	65.9	341	1	TAU3_MOUSE	P10637 mus musculu
5	1508	65.7	364	1	TAU2_MOUSE	P10638 mus musculu
6	1493	65.1	402	1	TAU3_BOVIN	P29173 bos taurus
7	863.5	37.6	0	1	TAU2_RAT	P15146 rattus norv
8	719.5	31.4	1861	1	MAP2_RAT	P15146 rattus norv
9	716	31.2	1828	1	MAP2_MOUSE	P20357 mus musculu
10	545	23.7	1152	1	MAP2_HUMAN	P11137 homo sapien
11	523.5	22.8	1125	1	MAP4_HUMAN	P27816 homo sapien
12	475	20.7	1072	1	MAP4_MOUSE	P27546 mus musculu
13	175.5	7.6	704	1	MAP4_BOVIN	P36225 bos taurus
14	175.5	7.6	857	1	NP14_RAT	P41777 rattus norv
15	163.5	7.1	825	1	NFM_CHICK	P16053 gallus gall
16	163.5	7.1	915	1	ICP0_HSV2H	P28284 herpes simp
17	161.5	7.0	670	1	NFM_HUMAN	P07197 homo sapien
18	161.5	7.0	831	1	VG50_HSV11	Q00130 ictalurid h
19	161	7.0	3924	1	NFM_RAT	P16884 rattus norv
20	160.5	7.0	1411	1	ANK2_HUMAN	Q01484 homo sapien
21	160	7.0	1487	1	TCOF_HUMAN	Q13428 homo sapien
22	158.5	6.9	1367	1	ICP4_HSVEB	P08640 equine herp
23	158	6.9	1487	1	AMYH_YEAST	P17473 saccharomyc
24	157	6.8	1906	1	ICP4_HSVEK	P27951 equine herp
25	156.5	6.8	699	1	BAG_STRAG	P27951 streptococc
26	155	6.8	1150	1	KMLS_CHICK	P13290 gallus gall
27	155	6.8	2805	1	VGLG_HSV2H	P13290 herpes simp
28	154.5	6.7	1446	1	APMU_PIG	P12021 sus scrofa
29	154	6.7	1664	1	MAPA_HUMAN	P78559 homo sapien
30	154	6.7	573	1	IE18_PRVKA	P33479 pseudorabie
31	153.5	6.7	1115	1	SLP1_CLOTM	Q06852 clostridium
32	152.5	6.7	1115	1	C114_MOUSE	P19467 mus musculu
33	152	6.6	1029	1	NCA1_MOUSE	P13595 mus musculu
34	151.5	6.6	1020	1	BCA_STRAG	Q02192 streptococc
35	151.5	6.6	1020	1	NFH_HUMAN	P12036 homo sapien
36	151	6.6	1650	1	CA2B_MOUSE	Q64739 mus musculu
37	150.5	6.6	2468	1	MAPB_HUMAN	P46821 homo sapien
38	150	6.5	1210	1	AF4_HUMAN	P51825 homo sapien
39	149.5	6.5	1453	1	CA11_CHICK	P02457 gallus gall
40	149	6.5	783	1	FYB_HUMAN	O15117 homo sapien
41	149	6.5	1183	1	DRPL_RAT	P54258 rattus norv
42	149	6.5	1275	1	TRP_DROME	P19334 drosophila
43	148.5	6.5	329	1	CCO6_CAEEL	P18831 caenorhabdi
44	148.5	6.5	817	1	VRP1_YEAST	P37370 saccharomyc
45	148	6.4	308	1	CC40_CAEEL	P34804 caenorhabdi

ALIGNMENTS

RESULT 1
TAU_HUMAN

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ID   TAU_HUMAN      STANDARD;      PRT;    441 AA.
AC   P10636; P18518; Q14799; Q15551;
DT   01-JUL-1989 (Rel. 11, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN TAU.
GN   MAPT OR MTBT1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89041757.
RA   Andreadis A., Brown W.M., Kosik K.S.;
RT   "Structure and novel exons of the human tau gene.";
RL   Biochemistry 31:10626-10633(1992).
RN   [2]
RP   SEQUENCE OF 1-44 AND 103-441 FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 93041757.
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89251564.
RA   Goedert M., Spillantini M.G., Potier M.C., Ulrich J., Crowther R.A.;
RT   "Cloning and sequencing of the cDNA encoding an isoform of
RT   microtubule-associated protein tau containing four tandem repeats:
RT   differential expression of tau protein mRNAs in human brain.";
RL   EMBO J. 8:393-399(1989).
RN   [3]
RP   SEQUENCE OF 1-26 AND 306-441 FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 88234557.
RA   Goedert M., Wischik C., Crowther R., Walker J., Klug A.;
RT   "Cloning and sequencing of the cDNA encoding a core protein of the
RT   paired helical filament of Alzheimer disease: identification as the
RT   microtubule-associated protein tau.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
RN   [4]
RP   SEQUENCE OF 1-26 AND 306-441 FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90180482.
RA   Lee G., Neve R.L., Kosik K.S.;
RT   "The microtubule binding domain of tau protein.";
RL   Neuron 2:1615-1624(1989).
CC   -!- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC       MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC   -!- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
CC       BY CAMP KINASE.
CC   -!- DISEASE: TAU CONSTITUTES AT LEAST A PART OF THE PAIRED HELICAL
CC       FILAMENT (PHF) CORE IN ALZHEIMER DISEASE.
CC   -!- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
CC   -!- DATABASE: NAME=HotMolecBase; NOTE=Tau entry;
CC       WWW="http://bioinformatics.weizmann.ac.il/hotmolecbase/entries/tau.htm".
```

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CC   -----------------------------------------------------------------------
DR   EMBL; AF027491; AAC04279.1; -.
DR   EMBL; AF047856; AAC04279.1; JOINED.
DR   EMBL; AF047857; AAC04279.1; JOINED.
DR   EMBL; AF027495; AAC04279.1; JOINED.
DR   EMBL; AF027496; AAC04279.1; JOINED.
DR   EMBL; AF027493; AAC04279.1; JOINED.
DR   EMBL; AF047863; AAC04279.1; JOINED.
DR   EMBL; AF047863; AAC04279.1; JOINED.
DR   EMBL; AF027491; AAC04279.1; JOINED.
DR   EMBL; AF027492; AAC04279.1; JOINED.
DR   EMBL; AF027492; AAC04279.1; JOINED.
DR   EMBL; AF027493; AAC04279.1; JOINED.
DR   EMBL; AF047860; AAC04278.1; JOINED.
DR   EMBL; AF047862; AAC04278.1; JOINED.
DR   EMBL; AF027495; AAC04278.1; JOINED.
DR   EMBL; AF027496; AAC04278.1; JOINED.
DR   EMBL; AF047863; AAC04278.1; JOINED.
DR   EMBL; J03778; AAA60615.1; -.
DR   EMBL; X14474; CAA32636.1; -.
DR   PIR; A30217; QRHUT1.
DR   PIR; PN0001; QRHUT2.
DR   PIR; S03796; S03796.
DR   MIM; 157140; -.
DR   PFAM; PF00418; tubulin-binding; 4.
DR   PROSITE; PS00229; TAU_MAP_1; 4.
KW   Microtubules; Repeat; Alternative splicing; Phosphorylation.
FT   REPEAT      244    274       TAU/MAP MOTIF.
FT   REPEAT      275    305       TAU/MAP MOTIF.
FT   REPEAT      306    336       TAU/MAP MOTIF.
FT   REPEAT      337    368       TAU/MAP MOTIF.
FT   DISULFID    291    322       BY SIMILARITY.
FT   VARSPLIC     45    102       MISSING (IN ISOFORM 3).
FT   VARSPLIC    275    305       MISSING (IN ISOFORM 1 AND ISOFORM 3).
FT   VARSPLIC      1     44       MAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDA
FT                                GLK -> MLRALQQRKR (IN FETAL ISOFORM).
FT   VARSPLIC    278    308       MISSING (IN FETAL ISOFORM).
SQ   SEQUENCE   441 AA;  45850 MW;  835A87D6D847A8CC CRC64;
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Query Match         98.6%;  Score 2262;  DB 1;  Length 441;
Best Local Similarity   99.1%;  Pred. No. 2.3e-101;
Matches  439;  Conservative  0;  Mismatches  0;  Indels  4;  Gaps  2;

Qy      1  MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE  58
           ||||||||||||||||  ||||||||||||||||  ||||||||||||||||||||||||
Db      1  MAEPRQEFEVMEDHAG--TYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEE  58

Qy     59  PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     59  PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118

Qy    119  AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    119  AGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPA 178

Qy    179  PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 238
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    179  PKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS 238

Qy    239  AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239  AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK 298
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Qy    299  HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299  HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD 358

Qy    359  NIIHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359  NIIHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID 418

Qy    419  MVDSPQLATLADEVSASLAKQGL 441
           |||||||||||||||||||||||
Db    419  MVDSPQLATLADEVSASLAKQGL 441
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```
RESULT   2
ID   TAU1_BOVIN     STANDARD;      PRT;   448 AA.
AC   P29172;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN TAU FORMS 1 AND 2.
GN   MAPT.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89261755.
RA   Himmler A., Drechsel D., Kirschner M.W., Martin D.W. Jr.;
RT   "Tau consists of a set of proteins with repeated C-terminal
RT   microtubule-binding domains and variable N-terminal domains.";
RL   Mol. Cell. Biol. 9:1381-1388(1989).
CC   -!- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC       MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC   -!- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
CC       BY CAMP KINASE.
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   -----------------------------------------------------------------------
DR   EMBL; L34953; AAA51609.1; -.
DR   EMBL; L34940; AAA51609.1; JOINED.
DR   EMBL; L34941; AAA51609.1; JOINED.
DR   EMBL; L34942; AAA51609.1; JOINED.
DR   EMBL; L34943; AAA51609.1; JOINED.
DR   EMBL; L34944; AAA51609.1; JOINED.
DR   EMBL; L34945; AAA51609.1; JOINED.
DR   EMBL; L34946; AAA51609.1; JOINED.
DR   EMBL; L34947; AAA51609.1; JOINED.
DR   EMBL; L34948; AAA51609.1; JOINED.
DR   EMBL; L34949; AAA51609.1; JOINED.
DR   EMBL; L34950; AAA51609.1; JOINED.
DR   EMBL; L34951; AAA51609.1; JOINED.
DR   EMBL; L34952; AAA51609.1; JOINED.
DR   EMBL; M26157; AAA30770.1; -.
DR   PIR; A31939; QRBOT1.
DR   PFAM; PF00418; tubulin-binding; 4.
DR   PROSITE; PS00229; TAU_MAP_1; 4.
KW   Microtubules; Repeat; Alternative splicing.
FT   REPEAT      251    281       TAU/MAP MOTIF.
FT   REPEAT      282    312       TAU/MAP MOTIF.
FT   REPEAT      313    343       TAU/MAP MOTIF.
FT   REPEAT      344    375       TAU/MAP MOTIF.
FT   VARSPLIC    175    192       MISSING (IN ISOFORM 2).
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SQ   SEQUENCE   448 AA; 46332 MW; 82163A9C4809602 CRC64;

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Query Match        87.6%;  Score 2011.5;  DB 1;  Length 448;
Best Local Similarity  86.7%;  Pred. No. 1.9e-89;
Matches 399;  Conservative 9;  Mismatches 21;  Indels 31;  Gaps 4;

Qy    1 MAEPRQEFEVMEDHAGDQTYGLDRKDQGGYTMH-QEGDTDAGLKESPLQTPTEDGSEEP 59
          |||||||| :|||||          |||||| |||||||||||||
Db    1 MAEPRQEFFDVMEDHA---------QGDYTLQDQEGDMDPGLKESPLQTPADDGSEEP 48

Qy   60 GSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAA 119
          ||||||||||||||| :||||||||||:||||| :|||||||:||||||||||| ::||
Db   49 GSETSDAKSTPTAEDATAPLVDEGAPGEQAAAQAPAEIPEGTAAEEAGIGDTSNLEDQAA 108

Qy  120 GHVTQARMVSKSKDGTGSDDKKAKGADGK--TKIATPRGAAPPGGQKGQANATRIPAKTPP 177
          ||||||||||| ||||| ||||:||||||  |||||||||||| |||||||||||||||
Db  109 GHVTQARMVSKGKDGTGPDDKKTKGADGKPGTKIATPRGAAPPGQKGQANATRIPAKTP 168

Qy  178 APKTPPSS----------------GEPPKSGDRGSYSSSPGSGPGTPGSRSRTPSLPTPPTR 221
          .|| |::               |||||||||| ||||||||| |||||||||||||||||
Db  169 TPKTSPATMQVKPPAGKPPAGAKSERGESGKSGDRSGYSSSPGSPGTPGSRSRTPSLPTPPTR 228

Qy  222 EPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKK 281
          |||||||||||||||||||||||:||  ||||||||||||||||||||||||||||||||
Db  229 EPKKVAVVRTPPKSPSSAKSRLQAAPGPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKK 288

Qy  282 LDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKS 341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  289 LDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKS 348

Qy  342 EKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSG 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  349 EKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSG 408

Qy  402 DTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL 441
          ||||||||||||||||||||||||||||||||||||||||
Db  409 DTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL 448
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RESULT 3

ID   TAU_RAT   STANDARD;   PRT;   432 AA.
AC   P19332;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN TAU.
GN   MAPT OR MTAP1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90180457.
RA   Kosik K.S., Orecchio L.D., Bakalis S., Neve R.L.;
RT   "Developmentally regulated expression of specific tau sequences.";
RL   Neuron 2:1389-1397(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89355509.
RA   Kanai Y., Takemura R., Oshima T., Mori H., Ihara Y., Yanagisawa M.,
RA   Masaki T., Hirokawa N.;
RT   "Expression of multiple tau isoforms and microtubule bundle formation
RT   in fibroblasts transfected with a single tau cDNA.";
RL   J. Cell Biol. 109:1173-1184(1989).
CC   -!- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC   MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC   PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC   -!- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED

CC   -!- BY CAMP KINASE.
CC   -!- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
DR   PIR; JS0306; JS0306.
DR   PIR; A33574; A33574.
DR   PROSITE; PS00229; TAU_MAP_1; 4.
DR   PFAM; PF00418; tubulin-binding; 4.
KW   Microtubule; Repeat; Alternative splicing; Phosphorylation.
FT   REPEAT   235   265   TAU/MAP MOTIF.
FT   REPEAT   266   296   TAU/MAP MOTIF.
FT   REPEAT   297   327   TAU/MAP MOTIF.
FT   REPEAT   328   359   TAU/MAP MOTIF.
FT   DISULFID   282   313   BY SIMILARITY.
FT   MOD_RES   347   347   PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   VARSPLIC   266   296   MISSING (IN FETAL ISOFORM).
SQ   SEQUENCE   432 AA; 45113 MW; A4810DF6CF04457F CRC64;

RESULT 4

ID   TAU3_MOUSE   STANDARD;   PRT;   341 AA.
AC   P10637;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN TAU (CLONE TA3).
GN   MAPT OR MTAP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 88809510.
RA   Lee G., Cowan N.J., Kirschner M.;
RT   "The primary structure and heterogeneity of tau protein from mouse
RT   brain.";

```
Query Match        87.3%;  Score 2003.5;  DB 1;  Length 432;
Best Local Similarity  88.1%;  Pred. No. 4.3e-89;
Matches 392;  Conservative 15;  Mismatches 21;  Indels 17;  Gaps 3;

Qy    1 MAEPRQEFEVMEDHAGDQTYGLDRKDQGGYTM-HQEGDTDAGLKESPLQTPTEDGSEE 58
          ||||||| :|||:|||          |||| |||||| ||| ||||||| :||||| |||
Db    1 MAEPRQEFDIMEDQAGD----------YTMLQDQEGDHDGLKESPQQPADDGSEE 47

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
          |||||||||||||||||||||:||  ||:|||:|  ||||||||||||||||||||:|:||
Db   48 PGSETSDAKSTPTAEDVTAPLVEEERAPDKQATAQSHTEIPEGTTAEEAGIGDTPNMEDQA 107

Qy  119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGGQKGQANATRIPAKTP 176
          ||||||| :  ||:|  |::|:||||||||||  |||||||||.|||||:||||||||||
Db  108 AGHVTQARVAVGVSKDRTGNDEKKAKGADGKTGAKIATPRGAATPGQKGTSNATRIPAKT 167

Qy  177 PAPKTPPSSGEPPKSGDRGSYSSSPGSGPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 236
          |:|||||.|||||||| | ||||||| |||||||||||||||||||||||||||||||||
Db  168 PSPKTPPGSGEPPKSGERSGYSSSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 227

Qy  237 SSAKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 296
          |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  228 SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 287

Qy  297 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  288 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 347

Qy  357 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  348 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 407

Qy  417 IDMVDSPQLATLADEVSASLAKQGL 441
          |||||||||||||||||||||||||
Db  408 IDMVDSPQLATLADEVSASLAKQGL 432
```

Left column

```
RL   Science 239:285-288(1988).
CC   -!- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC       MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC   -!- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
CC       BY CAMP KINASE.
CC   -!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC   -----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; M18775; AAA40165.1; -.
DR   PIR; B28820; B28820.
DR   MGD; MGI:97180; MTAPT.
DR   PFAM; PF00418; tubulin-binding; 3.
DR   PROSITE; PS00229; TAU_MAP_1; 3.
KW   Microtubules; Repeat; Alternative splicing.
FT   REPEAT      175    205       TAU/MAP MOTIF.
FT   REPEAT      206    236       TAU/MAP MOTIF.
FT   REPEAT      237    268       TAU/MAP MOTIF.
SQ   SEQUENCE   341 AA;   35714 MW;  478641931A5A4143 CRC64;

Query Match   65.9%;   Score 1512;   DB 1;   Length 341;
Best Local Similarity   69.7%;   Pred. No. 7.6e-66;
Matches 310;   Conservative 14;   Mismatches 13;   Indels 108;   Gaps 6;

Qy     1  MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTM--HQEGDTDAGLKESPLQTPTEDGSEE   58
          ||:|:||||.|||: ||||||                |||  | |||
Db     1  MADPRQEFDIMEDHAGD--------------------YTLLQDQEGDMDHGLK--------   33

Qy    59  PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA  118
                                                       |||||:|
Db    34  ----------------------------------------------AEEAGIGDTPNQEDQA   49

Qy   119  AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQKGQANATRIPAKTP  176
          ||||||||:|||:||||:||||||:|||||||  |||||||||   ||:||||||||||||
Db    50  AGHVTQARVA--SKDRTGNDEKKAKGADGKTGAKIATPRGAASPAQKGTSNATRIPAKTT  107

Qy   177  PAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP  236
          ||||||||||||:||:|||||||||:||||||||||||||||||||||||||||||||||
Db   108  PSPKTPPSSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP  167

Qy   237  SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN  296
          ::|||:|||||||||||||||:|||||||||||||||||
Db   168  SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGK----------------------  205

Qy   297  IKHVPGGGSVQIYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS  356
          ||||||||||||||||||||||||||||||||:|||||
Db   206  ------VOIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS    256

Qy   357  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS  416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   257  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS  316

Qy   417  IDMVDSPQLATLADEVSASLAKQGL  441
          |||||||||||||||||||||||||
Db   317  IDMVDSPQLATLADEVSASLAKQGL  341

RESULT 5
ID   TAU2_MOUSE    STANDARD;    PRT;    364 AA.
AC   P10638;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
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Right column

```
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN TAU (CLONE TA2).
GN   MAPT OR MTAPT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RL   Science 239:285-288(1988).
RA   Lee G., Cowan N.J., Kirschner M.;
RL   "The primary structure and heterogeneity of tau protein from mouse
RL   brain.";
RL   Science 239:285-288(1988).
CC   -!- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC       MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC   -!- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
CC       BY CAMP KINASE.
CC   -!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; M18776; AAA40166.1; -.
DR   PIR; A28820; A28820.
DR   MGD; MGI:97180; MTAPT.
DR   PFAM; PF00418; tubulin-binding; 3.
DR   PROSITE; PS00229; TAU_MAP_1; 3.
KW   Microtubules; Repeat; Alternative splicing.
FT   REPEAT      175    205       TAU/MAP MOTIF.
FT   REPEAT      206    236       TAU/MAP MOTIF.
FT   REPEAT      237    268       TAU/MAP MOTIF.
SQ   SEQUENCE   364 AA;   38199 MW;  D1CAB2EF89CDD7C0 CRC64;

Query Match   65.7%;   Score 1508;   DB 1;   Length 364;
Best Local Similarity   69.6%;   Pred. No. 1.3e-65;
Matches 309;   Conservative 14;   Mismatches 13;   Indels 108;   Gaps 6;

Qy     1  MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTM--HQEGDTDAGLKESPLQTPTEDGSEE   58
          ||:|:||||.|||: ||||||                |||  | |||
Db     1  MADPRQEFDIMEDHAGD--------------------YTLLQDQEGDMDHGLK--------   33

Qy    59  PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA  118
                                                       |||||:|
Db    34  ----------------------------------------------AEEAGIGDTPNQEDQA   49

Qy   119  AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQKGQANATRIPAKTP  176
          ||||||||:|||:||||:||||||:|||||||  |||||||||   ||:||||||||||||
Db    50  AGHVTQARVA--SKDRTGNDEKKAKGADGKTGAKIATPRGAASPAQKGTSNATRIPAKTT  107

Qy   177  PAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP  236
          ||||||||||||:||:|||||||||:||||||||||||||||||||||||||||||||||
Db   108  PSPKTPPSSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP  167

Qy   237  SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN  296
          ::|||:|||||||||||||||:|||||||||||||||||
Db   168  SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGK----------------------  205

Qy   297  IKHVPGGGSVQIYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS  356
          ||||||||||||||||||||||||||||||||:|||||
Db   206  ------VOIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS    256

Qy   357  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS  416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   357  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS  416
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Db    257  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 316
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    417  IDMVDSPQLATLADEVSASLAKOG 440
           ||||||||||||||||||||||||
Db    317  IDMVDSPQLATLADEVSASLAKQG 340
```

```
RESULT 6
ID   TAU3_BOVIN     STANDARD;       PRT;    402 AA.
AC   P29173;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN TAU FORMS 3, 4, AND 5.
GN   MAPT.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89261765.
RA   Himmler A., Drechsel D., Kirschner M.W., Martin D.W.Jr.;
RT   "Tau consists of a set of proteins with repeated C-terminal
RT   microtubule-binding domains and variable N-terminal domains.";
RL   Mol. Cell. Biol. 9:1381-1388(1989).
CC   -!- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC       MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC   -!- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
CC       BY CAMP KINASE.
CC   -!- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
CC   -------------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC       entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------
DR   EMBL; M26158; AAA30771.1; -.
DR   PIR; B31339; QRBOT2.
DR   PFAM; PF00418; tubulin-binding; 4.
DR   PROSITE; PS00229; TAU_MAP_1; 4.
KW   Microtubule; Repeat; Alternative splicing.
FT   REPEAT       205    235       TAU/MAP MOTIF.
FT   REPEAT       236    266       TAU/MAP MOTIF.
FT   REPEAT       267    297       TAU/MAP MOTIF.
FT   REPEAT       298    329       TAU/MAP MOTIF.
FT   VARSPLIC       1    100       MISSING (IN ISOFORM 4).
FT   VARSPLIC     235    296       MISSING (IN ISOFORM 5).
SQ   SEQUENCE   402 AA;   42232 MW;   A7FCED47A04D7340 CRC64;
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Qy    Query Match    65.1%;    Score 1493;    DB 1;    Length 402;
      Best Local Similarity   79.7%;   Pred. No. 7.2e-65;
Matches 303;   Conservative 14;   Mismatches 29;   Indels 34;   Gaps 6;
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Qy    64   SDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHEIPEGTIAEEAGIGDTPSLEDEAAGHVT 123
           |  || | ||    ||||  | |  |  |   |  || ||  | |||  | | | |:||
Db    55   SRKPTPGSSD----PLIKPSSP----------AVCPEPESSSPK--------------HVS 87
```

```
Qy    124  QARMVSKSRDGTGSDDKARGADGK--TKIATPRGAAPPGQKGQANATRIPAKTPAPKT 181
           |:| |      | ||  ||  |     |||| |  | ||| |    | | | ||  |||
Db    88   S----VIPRTGNSGAKEMKVGADGKPGTKIATPRGAAPPGQKGQANATRIPAKTTPTPKT 144
```

```
Qy    182  PSSGEEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAKS 241
           ||| | | | || |  | |||| |||||||| | | | |||| | | | | ||||||||
Db    145  SP--GESGKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSPSAKS 202
```

```
Qy    242  RLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVP 301
           |  |   | ||  | ||| ||||||||| | |||||||||||||||||||||||||||||
Db    203  RLQAAPGPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVP 262
```

```
Qy    302  GGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNIT 361
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    263  GGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNIT 322
```

```
Qy    362  HVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVD 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    323  HVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVD 382
```

```
Qy    422  SPQLATLADEVSASLAKQGL 441
           ||||||||||||||||||||
Db    383  SPQLATLADEVSASLAKQGL 402
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RESULT 7
ID   MAP2_RAT     STANDARD;       PRT;    1861 AA.
AC   P15146;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-OCT-1994 (Rel. 30, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN 2 (MAP2B) [CONTAINS: MAP2C].
GN   MAP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
RX   MEDLINE; 90251471.
RA   Kindler S., Schwanke B., Schulz B., Garner C.C.;
RT   "Molecular structure of microtubule-associated protein 2b and 2c from
RT   rat brain.";
RL   J. Biol. Chem. 265:19679-19684(1990).
RN   [2]
RP   SEQUENCE OF 1-151; 1515-1694 AND 1726-1861 FROM N.A.
RX   MEDLINE; 90221819.
RA   Doll T., Papandrikopoulou A., Matus A.;
RT   "Nucleotide and amino acid sequences of embryonic rat MAP2c.";
RL   Nucleic Acids Res. 18:361-361(1990).
RN   [4]
RP   DISCUSSION OF SEQUENCE.
RX   MEDLINE; 89365159.
RA   Papandrikopoulou A., Doll T., Tucker R.P., Garner C.C., Matus A.;
RT   "Embryonic MAP2 lacks the cross-linking sidearm sequences and
RT   dendritic targeting signal of adult MAP2.";
RL   Nature 340:650-652(1989).
RN   [5]
RP   SEQUENCE OF 1695-1725 FROM N.A.
RX   MEDLINE; 94110302.
RA   Doll T., Meichsner M., Riederer B.M., Honegger P., Matus A.;
RT   "An isoform of microtubule-associated protein 2 (MAP2) containing
RT   four repeats of the tubulin-binding motif.";
RL   J. Cell Sci. 106:633-640(1993).
CC   -!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
CC       STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
CC       SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
CC       FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
CC   -!- DEVELOPMENTAL STAGE: MAP2C IS EXPRESSED DURING EMBRYONIC BRAIN
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Left column

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AC   P20357;
ID   MAP2_MOUSE              STANDARD;        PRT;   1828 AA.
RESULT 8
MAP2_MOUSE
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Qy    415 GSIDMVDSPQLATLADEVSASLAKQGL 441
Db   1835 GSINLLESPQLATLAEDVTPALAKGL 1861

Qy   1775 GSLDNAHVPGGGNVKIDSQKLNFREHAKARVDHGAEIITQSPSRSSVASPRRLSNVSSS 1834

Qy    355 GSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSST 414

Qy    197 YSSPGSPG------TPGS------RSRTPSLPTPPT--REP------------KKVAVRTPPR 234
Db   1596 TSTPTTPGSTAITPGTPPSYSSRPGTPGTPSYPRTPGIPKSGILVPSEKRVAIRTPPK 1655

Qy    235 SPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSK 294
Db   1596 KEKPFKTGRGRISTPERREVAKKEPSTVSRDEVRRKAVYKKAELAKESEVQAHSPSRKL 1492

Qy     90 AAQPHTE------IPEGTTAEEAGIGDTPSLEDEAGHVTQARMVSKSKDGTGSDDK 140
Db   1493 ILKPAIKYTRPTHLSCVKRKITATSGESAQAPSAFKQAKDKVT----------DG 1537

Qy    141 KAKGADGKTKIATPRGAAP----GQKG--QANATRIPAKTPPAPKTPPSSGEPPKSGDRSG 196
Db    152 ITKSPEKRSSLPRPSSILPPRGVSGDREENSFSLNSSISSARRTRS--EPIRRAGKSG 1595

Qy     44 KESPLOT------------PTEDGSEEPGSETSDAKSTPTAEDVTAPLVDEG-----APGKQA 89
Db   1433 KEKPFKTGRGRISTPERREVAKKEPSTVSRDEVRRKAVYKKAELAKESEVQAHSPSRKL 1492
```

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SQ   SEQUENCE   1861 AA;  202409 MW;  42DCF116D21EF54E CRC64;
FT   VARSPLIC   1695  1725  MISSING (IN ISOFORM WITH 3 TAU/MAP
FT                          REPEATS).
FT   VARSPLIC   1514  1725  MISSING (IN ISOFORM MAP2C).
FT   VARSPLIC   152   1514  MISSING (IN ISOFORM MAP2C).
FT   REPEAT     1788        TAU/MAP MOTIF.
FT   REPEAT     1757  1788  TAU/MAP MOTIF.
FT   REPEAT     1726  1756  TAU/MAP MOTIF.
FT   REPEAT     1695  1725  TAU/MAP MOTIF.
FT   REPEAT     1664  1694  TAU/MAP MOTIF.
FT   DOMAIN     1454  1474  CALMODULIN-BINDING (POTENTIAL).
KW   Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
DR   PROSITE; PS00229; TAU_MAP_1; 3.
DR   PFAM; PF00418; tubulin-binding; 4.
DR   PIR; A37981; A37981.
DR   PIR; S10003; S10003.
DR   EMBL; S07887; S07887.
DR   EMBL; X71487; CAA50588.1; -.
DR   EMBL; X17682; CAA35567.1; -.
DR   EMBL; X51842; CAA36135.1; -.
```

Best Local Similarity 44.3%; Pred. No. 2.7e-34;

Query Match 37.6%;   Score 863.5; DB 1; Length 1861;
Matches 198; Conservative 67; Mismatches 115; Indels 67; Gaps 12;

```
CC   -!- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
DE   THROUGHOUT BRAIN DEVELOPMENT.
DE   DEVELOPMENT AND UNTIL POSTNATAL DAY 10. MAP2B IS EXPRESSED
```

Right column

```
Qy    297 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKRPGGGQVEVKSEKLDFKDRVQSKIGS 356
Db   1656 ATPK-QLRLINQPLPDLKNVKSKIGSTDNIKYQPRGGQVQIVTKRIDLSH----------- 1704

Qy    237 SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 296
Db   1656 ----------------------------------- 1655

Qy    181 TPPSSGEPPKSGDRSGYSS--PGSPGTPGSRSRPSLPTPPTREP----KKVAVRTPPRSP 236
Db   1609 TPPS------------------YSSRTPGTPGTP-SYPRTPGTPKSGILVPSEKRVAIRTPPKSP 1655

Qy    137 ---------------SDDKRAKGADGKTKIATPRGAA------PPGQKGQANATRIPAKTPPAPK 180
Db   1492 LKPAIKYTRPTHLSCVKRKITAASGDLAQAPGAFKQAKDKVTDG--ISKSPEKRSSLPRP 1549

Qy     91 AQPHTE------IPEGTTAEEAGIGDTPSLEDEAGHVTQARMVSKSKDGTG---- 136
Db   1432 KEKPFKTGRGRISTPERKVAKKEPSTVSRDEVRRKAVYKKAELAKKSEVQAHSPSRKLI 1491

Qy     44 KESPLOT------------PTEDGSEEPGSETSDAKSTPTAEDVTAPL-----VDEGAPGKQAA 90
Db   1432 KEKPFKTGRGRISTPERKVAKKEPSTVSRDEVRRKAVYKKAELAKKSEVQAHSPSRKLI 1491
```

```
SQ   SEQUENCE   1828 AA;  198980 MW;  200BC59E360538CA CRC64;
FT   REPEAT     1724  1755  TAU/MAP MOTIF.
FT   REPEAT     1693  1723  TAU/MAP MOTIF.
FT   REPEAT     1662  1692  TAU/MAP MOTIF.
FT   DOMAIN     1452  1472  CALMODULIN-BINDING (POTENTIAL).
KW   Microtubules; Repeat; Calmodulin-binding.
DR   PROSITE; PS00229; TAU_MAP_1; 2.
DR   PFAM; PF00418; tubulin-binding; 3.
DR   MGD; MGI:97175; MTAP2.
DR   PIR; A40115; A40115.
DR   PIR; S06467; S06467.
DR   EMBL; M21041; AAA39490.1; -.
```

Best Local Similarity 39.6%; Pred. No. 1.8e-27;

Query Match 31.4%;   Score 719.5; DB 1; Length 1828;
Matches 176; Conservative 61; Mismatches 113; Indels 95; Gaps 13;

```
CC   -!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC       SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC       STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
CC   -!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
RL   Science 242:936-939(1988).
RX   MEDLINE; 89043973.
RA   Lewis S.A., Wang D., Cowan N.J.;
RT   "Microtubule-associated protein MAP2 shares a microtubule binding
RT   motif with tau protein.";
RP   SEQUENCE FROM N.A.
RL   Nucleic Acids Res. 16:11369-11370(1988).
RX   MEDLINE; 89083571.
RA   Wang D., Lewis S.A., Cowan N.J.;
RT   "Complete sequence of a cDNA encoding mouse MAP2.";
RP   SEQUENCE FROM N.A.
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS   Mus musculus (Mouse).
GN   MAP2 OR MTAP2.
DE   MICROTUBULE-ASSOCIATED PROTEIN 2.
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-FEB-1991 (Rel. 17, Created)
```

```
Db 1705 ----------- |||||||| || |:|:|||| |||:|||||||||:|| |:|:||
                    -VTSKCGSLKNIRHRPGGGRVKIESVKLDFKEKAQAKVGS 1743
Qy  357 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416
Db 1744 LDNAHHVPGGGNVKIDSOKLNFREHAKARVDHGAEIITQSPSRSSVASPPRLSNVSSSGS 1803
Qy  417 IDMVDSPQLATLADEVSASALAKQGL 441
        |:||||||||||||:|:|:||||||||
Db 1804 INLLESPQLATLAEDVTAALAKOGL 1828
```

RESULT 9
MAP2_HUMAN

```
ID   MAP2_HUMAN    STANDARD;    PRT;   1827 AA.
AC   P11137; Q99976; Q99975;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN 2 (MAP2B) [CONTAINS: MAP2C].
GN   MAP2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Price R.;
RL   Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX   MEDLINE; 94124038.
RA   Albala J.S., Kalcheva N., Shafit-Zagardo B.;
RT   "Characterization of the transcripts encoding two isoforms of human
RT   microtubule-associated protein-2 (MAP-2).";
RL   Gene 136:377-378(1993).
RN   [3]
RP   SEQUENCE OF 493-1562 FROM N.A.
RX   MEDLINE; 88274407.
RA   Kosik K.S., Orecchio L.D., Bakalis S., Duffy L., Neve R.L.;
RT   "Partial sequence of MAP2 in the region of a shared epitope with
RT   Alzheimer neurofibrillary tangles.";
RL   J. Neurochem. 51:587-598(1988).
-!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
    STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
    SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
-!- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
    ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
    FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
-!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
```

```
DR   EMBL; U01828; AAA03354.1; -.
DR   EMBL; U89330; AAB48098.1; -.
DR   EMBL; U89329; AAB48097.1; -.
DR   EMBL; M25668; AAA59552.1; -.
DR   PIR; PL0024; QRHUMT.
     MIM; 157130;
DR   PFAM; PF00418; tubulin-binding; 3.
DR   PROSITE; PS00229; TAU_MAP_1; 2.
KW   Microtubule; Repeat; Alternative splicing; Calmodulin-binding.
DOMAIN    1447  1467    CALMODULIN-BINDING (POTENTIAL).
DOMAIN    1661  1691    TAU/MAP MOTIF.
REPEAT    1692  1722    TAU/MAP MOTIF.
REPEAT    1723  1754    TAU/MAP MOTIF.
VARSPLIC  152   1507    MISSING (IN ISOFORM MAP2C).
```

```
FT   CONFLICT    9     9      A -> G (IN REF. 2).
FT   CONFLICT    37    37     R -> A (IN REF. 2).
FT   CONFLICT    108   108    A -> G (IN REF. 2).
FT   CONFLICT    152   155    MISSING (IN REF. 2).
FT   CONFLICT    187   187    S -> K (IN REF. 2).
FT   CONFLICT    1655  1655   S -> K (IN REF. 2).
FT   CONFLICT    1736  1736   V -> GL (IN REF. 2).
FT   CONFLICT    1736  1736   V -> A (IN REF. 2).
SQ   SEQUENCE   1827 AA;  199610 MW;  BAC36D00330F5F455 CRC64;
```

```
Query Match   31.2%;  Score 716;  DB 1;  Length 1827;
Best Local Similarity   36.9%;  Pred. No. 2.7e-27;
Matches  191;  Conservative  75;  Mismatches  132;  Indels  120;  Gaps  19;

Qy    2 AEPRQEFEEVMEDHAGQDTYGLGDRKDQ------GGYTMHOEG------DTDAGLKESPLQT-P 51
Db 1352 ASPERE-EVALSEYKIETY--DDYKDETTIDDSIMDADSLWVDTQDDDRSIMTEQLETIP 1408
Qy   52 TEDGSEEPGSETSDAK------------STP----TAEDVTAPLVDE----GAPGKQA 89
Db 1409 KEEKAEKEARRSSLEKHRKEKPFKTGRGRISTPERKVAKKEPSTVSRDEVRRKKAYYKKA 1468
Qy   90 AAQPHFIPEGTTAEFAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGS------DDKKAK 143
Db 1469 ELAKKIEVQAHSPSRKFIL--KPAIKYTRPTHLSCVKRKITAAGGESALAPSVFKQAKDK 1526
Qy  144 GADGKTKIATPRGAAP-------PGQKG-----------QANATRIPAKTP---- 176
Db 1527 VSDGVTKSPEKRSSLPRPSSILPPRRGVSGDRDENSFSLNSSISSSARRTTRSEPIRRAG 1586
Qy  177 ----PAPKTPPSS---GEPPKSGDRSGYSSPGSPGTPGPGSRSRTPSLPTP----TREP 223
Db 1587 KSGTSITPTTPGSTAIFPGTPPSYSSR----TPGTPGTP-SYPRTPHTPGTPKSAILVPSE 1641
Qy  224 KVAVAVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKLD 283
Db 1642 KKVAIIRIPPKSPATPK-QLRLINQPLPDLKNVKSKIGSTDNIKIYQPKGGQVQIVTKKID 1700
Qy  284 LSNVQSKCGSKDNIKIHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGOVEVKSEK 343
Db 1701 LSH------VTSKCGSLKNIRHRPGGGRVKIESVK 1729
Qy  344 LDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDT 403
Db 1730 LDFKEKVQAKVGSLDNAHHVPGGGNVKIDSOKLNFREHAKARVDHGAEIITQSPGRSSVA 1789
Qy  404 SPRHLSNVSSTGSIDMVDSPQLATLADEVSASALAKQGL 441
Db 1790 SPRRLSNVSSGSINLLESPQLATLAEDVTRALAKOGL 1827
```

RESULT 10
MAP4_HUMAN

```
ID   MAP4_HUMAN    STANDARD;    PRT;   1152 AA.
AC   P27816;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN 4.
GN   MAP4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92042100.
RA   West R.R., Tenberge K.M., Olmsted J.B.;
RT   "A model for microtubule-associated protein 4 structure. Domains
RT   defined by comparisons of human, mouse, and bovine sequences.";
RL   J. Biol. Chem. 266:21886-21896(1991).
RN   [2]
RP   SEQUENCE OF 102-1152 FROM N.A.
RC   TISSUE=BRAIN;
```

```
RX   MEDLINE; 91277031.
RA   Chapin S.J.; Bulinski J.C.;
RT   "Non-neuronal 210 x 10(3) Mr microtubule-associated protein (MAP4)
RT   contains a domain homologous to the microtubule-binding domains of
RT   neuronal MAP2 and tau.";
RL   J. Cell Sci. 98:27-36(1991).
CC   -!- FUNCTION: NON-NEURONAL MICROTUBULE-ASSOCIATED PROTEIN. PROMOTES
CC       MICROTUBULE ASSEMBLY.
CC   -!- PTM: PHOSPHORYLATION OF THE PRO-RICH REGION IN THE C-TERMINUS
CC       NEGATIVELY REGULATES MAP-4 ACTIVITY TO PROMOTE MICROTUBULE
CC       ASSEMBLY.
CC   -!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
```

```
DR   EMBL; M64571; AAA59553.1; -.
DR   PIR; A33183; A33183.
DR   PIR; A41206; A41206.
MIM; 157132; -.
KW   Microtubules; Repeat; Phosphorylation; Alternative splicing.
PROSITE; PS00229; TAU_MAP_1; 4.
PFAM; PF00418; tubulin-binding; 4.
FT   DOMAIN    248  545   17 X 14 AA TANDEM REPEATS.
FT   REPEAT    248  261   1.
FT   REPEAT    262  275   2.
FT   REPEAT    274  289   3.
FT   REPEAT    290  303   4.
FT   REPEAT    304  317   5.
FT   REPEAT    318  331   6.
FT   REPEAT    332  345   7.
FT   REPEAT    346  351   8 (INCOMPLETE).
FT   REPEAT    352  377   26 RESIDUES 1.
FT   REPEAT    378  403   26 RESIDUES 2.
FT   REPEAT    408  421   9.
FT   REPEAT    422  433   10.
FT   REPEAT    434  447   11.
FT   REPEAT    448  461   12.
FT   REPEAT    462  475   13.
FT   REPEAT    476  489   14.
FT   REPEAT    490  503   15.
FT   REPEAT    504  517   16.
FT   REPEAT    532  545   17.
FT   REPEAT    923  953   TAU/MAP MOTIF.
FT   REPEAT    992 1022   TAU/MAP MOTIF.
FT   REPEAT   1023 1053   TAU/MAP MOTIF.
SQ   SEQUENCE   1152 AA;  121180 MW;  0B6CF0CF926B558F CRC64;
```

```
Query Match  23.7%;  Score 545;  DB 1;  Length 1152;
Best Local Similarity  30.4%;  Pred. No. 2.3e-19;
Matches 165;  Conservative 58;  Mismatches 160;  Indels 160;  Gaps 18;

Qy      4  PRQEEVEMEDHAGQDTYGLGDRK------------------DQGGYTMHQEGD----------TDAG 42
             ||  |:|                                                   |  |||
Db    638  PAEEDSVLEK-------LGERKPCNSQPSELSSEETSGIARPEEGRPVVSGGTGNDIITPP 689

Qy     43  LKESPLQTPPEDGSEEP---------GSETSDAKSTPTA----------------EDVTAP 78
             ||:  :| :                ||  | :|:                       :|
Db    690  NKELP---PSPEKKIKPLATTQPAKTSTSRAKTQPTSLPKQPAPTIIGGLNKKPMSLASG 746

Qy     79  LVDEGAPGKQAAAQPHEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSD 138
             |:|     :|  :|   |  | |  ||: |||  ||   || |:  |     |   |
Db    747  LVPAAPPKRPAVASARPSILPSKDVKPKPIADAKAPEKRASPSKPASPASRS---GS- 801

Qy    139  DKKAGADGKTKIATPRGAPPGKQGQANATRIPAKTPPPAPKTPPSSGEPPKSGDRS--- 195
             |:|    : |||:     :     :||| |  ||  ||     | |:  |:||
Db    802  ----KSTQTVAKTTTAAAVASTGPSSRSPSTLLP-KPTAIKTEGKRPAEVKKMTAKSVPA 856
```

```
RESULT 11
MAP4_MOUSE
ID   MAP4_MOUSE     STANDARD;     PRT;     1125 AA.
AC   P27546;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN 4.
GN   MAP4 OR MTAP4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92042100.
RA   West R.R., Tenbarge K.M., Olmsted J.B.;
RT   "A model for microtubule-associated protein 4 structure. Domains
RT   defined by comparisons of human, mouse, and bovine sequences.";
RL   J. Biol. Chem. 266:21886-21896(1991).
CC   -!- FUNCTION: NON-NEURONAL MICROTUBULE-ASSOCIATED PROTEIN. PROMOTES
CC       MICROTUBULE ASSEMBLY.
CC   -!- TISSUE SPECIFICITY: TESTIS, STRIATED AND CARDIAC MUSCLE.
CC   -!- PTM: PHOSPHORYLATION OF THE PRO-RICH REGION IN THE C-TERMINUS
CC       NEGATIVELY REGULATES MAP-4 ACTIVITY TO PROMOTE MICROTUBULE
CC       ASSEMBLY.
CC   -!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
```

```
DR   EMBL; M72414; AAA16372.1; -.
DR   PIR; B41206; B41206.
MGD; MGI:97178; MTAP4.
PROSITE; PS00229; TAU_MAP_1; 4.
PFAM; PF00418; tubulin-binding; 4.
KW   Microtubules; Repeat; Phosphorylation.
FT   REPEAT    896  926   TAU/MAP MOTIF.
FT   REPEAT    965  995   TAU/MAP MOTIF.
FT   REPEAT    996 1026   TAU/MAP MOTIF.
SQ   SEQUENCE   1125 AA;  117675 MW;  73047432A329AA1D CRC64;

Qy    196  GYSSPGSPGTPGSSRSRPSLPTPPTR--------EPRKVAVRTP-----------PRSPSSAR---- 240
                |||| | ::   | |  | |          |  |:  |            | |:|||
Db    857  DLSRPKSTSTSSMKKTTTLSGTAPAGVVPSRVKATPMPSRPSTTPIDKPTSAKPSST 916

Qy    241  ----SRLQTAPVPMPDLKNVSKIGSTENLKHQPGG------------------------ 272
               |||:|||||||||||||||||||||||||
Db    917  TPRLSRLAT-NTSAPDLKNVRSKVGSTENIKHQPGGGRAKVEKKTEAAATTRKPESNAVT 975

Qy    273  ---------GRYQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIYTKPVDLSKV 318
                     |||||||||||||||||||||||||||||||||:|||  |||||
Db    976  KTAGPIASAQKQPAGRKVQIVSRKVSYSHIQSKCGSKDNIKHVPGGGNVQIQNKKVDISKV 1035

Qy    319  TSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTF 378
             ||||| :| ||||||| ||:||| ||:||  | | | | || |||||| | |:   | |
Db   1036  SSKCGSKANIKHKPGGGDVKIESQKLNFKERAQAKVGSLDNVGHLPAGG---------- 1084

Qy    379  RENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAK 438
              |||:|||  |||:   :|| :  |   | || ::    || |   ||  ||
Db   1085  ---AVKTEGGGS---EAPLCPGPPAG-----------------EEPAISEAAPEAGAPTSA 1122

Qy    439  QGL 441
             |||
Db   1123  SGL 1125
```

```
Query Match     22.8%;  Score 523.5;  DB 1;  Length 1125;
Best Local Similarity 33.9%;  Pred. No. 2.3e-18;
Matches 149;  Conservative 51;  Mismatches 128;  Indels 111;  Gaps 14;

Qy    44 KESPLQTPTEDGSEEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQP-HTEIPEGTT 102
Db   625 KETPGSQPSEPCSGVSRQEEAKAANVGTVGNDITTPPNKEPPSPEKKAKPLATTQPAKTS 684

Qy   103 AEEA------------------GIGDP-----SLEDEAAGHVTQARMVSKSKDGT--GSDD 139
Db   685 TSKAKTQPTSLPKQPAPTSGGLNKPMSLASGSVPAAPHKRPAAATATARPSTLPARDV 744

Qy   140 K-----KAKGADGKTKIATPRG--AAPPGQK-----------------GQANATRIPAKT-P 176
Db   745 KPRPIPEAKVAEKRPSPSKPSSSAPALKPGKPRTTPPTVSKATSPSTLVSTGPSSRSPATTLP 804

Qy   177 PAPKTPPSSGEP----------PKSGDRSGSYSSPGSPGTPGSSRTPSLPTPP-----TR--- 221
Db   805 KRPTSIKTEGKPADVKRMTAKSASADLSRSKTTSASSVKRNTPTPGAAPGMISTRVKP 864

Qy   222 --EPKVAVVRTPPRSPSSAX------SRLQTAPVPMPDLKNVKSKIGSTENLKHQPG 271
Db   865 MSAPSRSSGALSVDKKPTSTKPSSSAPRVSRLATT-VSAPDLKSVRSKVGSTENIKHQPG 923

Qy   272 G----------------------GKVQIINKKLDLSNVQSKKCGS 293
Db   924 GGRAKVEKKTEAATTAGKPEPNAVTKAAGSTASAQKPPAGRVQIVSKKVSYSHIQSKCVS 983

Qy   294 KDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGG 353
Db   984 KDNIKHVPGGCNVQIONKKVDISKVSSKCGSKANIKHKPGGGDVKIESQKLNFKEKAQAK 1043

Qy   354 IGSLDNITHYPGGGNKKIE 372
Db  1044 VGSLDNVGHPPAGGAVKTE 1062


RESULT 12
MAP4_BOVIN
ID   MAP4_BOVIN     STANDARD;     PRT;     1072 AA.
AC   P36225;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN 4 (MICROTUBULE-ASSOCIATED PROTEIN-U)
DE   (MAP-U).
GN   MAP4.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE; 90338002.
RA   Aizawa H., Emori Y., Murofushi H., Kawasaki H., Sakai H.,
RA   Suzuki K.;
RT   "Molecular cloning of a ubiquitously distributed
RT   microtubule-associated protein with Mr 190,000.";
RL   J. Biol. Chem. 265:13849-13855(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91236765.
RA   Aizawa H., Mori A., Murofushi H., Sakai H., Suzuki K.;
RT   "Functional analyses of the domain structure of
RT   microtubule-associated protein-4 (MAP-U).";
RL   J. Biol. Chem. 266:9841-9846(1991).
CC   -!- FUNCTION: NON-NEURONAL MICROTUBULE-ASSOCIATED PROTEIN. PROMOTES
CC       MICROTUBULE ASSEMBLY.
CC   -!- TISSUE SPECIFICITY: IS DISTRIBUTED UBIQUITOUSLY AMONG ALL TISSUES
CC       BUT AMOUNTS ARE LOWER IN CEREBELLUM AND LIVER.
CC   -!- PTM: PHOSPHORYLATION OF THE PRO-RICH REGION IN THE C-TERMINUS
CC       NEGATIVELY REGULATES MAP-4 ACTIVITY TO PROMOTE MICROTUBULE
CC       ASSEMBLY.
CC   -!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; D90149; BAA14179.1; -.
DR   PIR; A37127; A37127.
DR   PFAM; PF00418; tubulin-binding; 3.
DR   PROSITE; PS00229; TAU_MAP_1; 3.
KW   Microtubule; Repeat; Phosphorylation.
FT   DOMAIN      244    530       19 X 14 AA TANDEM REPEATS.
FT   REPEAT      244    257       1.
FT   REPEAT      258    271       2.
FT   REPEAT      272    285       3.
FT   REPEAT      286    299       4.
FT   REPEAT      300    313       5.
FT   REPEAT      314    327       6.
FT   REPEAT      328    341       7.
FT   REPEAT      342    355       8.
FT   REPEAT      384    391       9 (INCOMPLETE).
FT   REPEAT      392    405       10.
FT   REPEAT      406    417       11.
FT   REPEAT      418    431       12.
FT   REPEAT      432    445       13.
FT   REPEAT      446    460       14.
FT   REPEAT      461    474       15.
FT   REPEAT      475    488       16.
FT   REPEAT      489    502       17.
FT   REPEAT      503    516       18.
FT   REPEAT      517    530       19.
FT   TAU/MAP MOTIF.
FT   TAU/MAP MOTIF.
FT   TAU/MAP MOTIF.
FT   TAU/MAP MOTIF.
SQ   SEQUENCE   1072 AA;   111914 MW;   E8C17A730989F0D2 CRC64;


Query Match     20.7%;  Score 475;  DB 1;  Length 1072;
Best Local Similarity 31.7%;  Pred. No. 4.4e-16;
Matches 145;  Conservative 53;  Mismatches 132;  Indels 128;  Gaps 20;

Qy    32 TMHQEGDTDAGLKESP----------LQTPIEDGS------EEPGSETSDAKSTPTAEDV 75
Db   558 SLQDEQSAVPLMTSPEAVVAMQQKHISLPTDEDSVLEELEQGKKPSSQTSELPSETSG--V 615

Qy    76 TAPLVDEGAP-------GKQAAAQPHTEIPEGTTAEEAGIGDPTPSLEDEAAGHVTQARMVSK 130
Db   616 AKP--EEGPPTGSVSGNDITAPPNKELPPSPEKKIKPLATTQPAKTSTSRAKTQPTSLPK 673

Qy   131 SKDGT---GSDDKKAKGADGKTKIATPRGAAPPGQKGQANA--TRIPAK-TPPAP----K 180
Db   674 QTAPTTLGGSNKKPMSLASGSVP------AAPPKRPAAAATSRPSTLPSKDTKPKPVAEAK 727

Qy   181 TP------------PSSGEPPKSGDRSGYSSPGSPGT------PGSRSRPSLPTP--PT----- 220
Db   728 IPEKRVSPSRPASAPAVKPGSKSTQAVPKRAPATATLASPGSTSRNLSTPLPKRPTAIKTE 787

Qy   221 ---REPKKVAVVRTP------PKS----------------PSSAKSRLQ-----TAPVP-- 249
Db   788 GKPAEIKKMATKSAPADLSRPKSTTTSSVKKSTTVPGTAPPAGAPSRARPTATPPRRPSGT 847

Qy   250 --------------MPDLKNVKSKIGSTENLKHQPGGGKVQIINKKL 282
Db   848 PPVDKKPTAAKPTSSAPRLGRVAANASAPDLKNVRSKVGSTENIKHQPGGGRAK-VEKKT 906

Qy   283 DLS-------NVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGG 334
Db   907 EAAAPARKPEPNAVTKAAGPIGNAQKPPTGKVQIQNKKVDISKVSSKCGSKANIKHKPGG 966
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Qy  335  GQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIE 372
         |::|::|||:|::||:||||:||||||||||||||| |
Db  967  GDVKIESQKLNFKEKAQAKVGSLDNVGHLPAGGAVKTE 1004


RESULT 13
NP14_RAT
ID   NP14_RAT    STANDARD;    PRT;   704 AA.
AC   P41777;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   140 KDA NUCLEOLAR PHOSPHOPROTEIN (NOPP140).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 292-309 AND 563-601.
RC   TISSUE=LIVER;
RX   MEDLINE; 92323542.
RA   Meier U.T., Blobel G.;
RL   "Nopp140 shuttles on tracks between nucleolus and cytoplasm.";
RL   Cell 70:127-138(1992).
-!- FUNCTION: MAY FUNCTION AS A CHAPERONE FOR IMPORT INTO AND/OR FROM
CC   THE NUCLEOLUS. IT COULD FUNCTION TO COVER AND NEUTRALIZE HIGHLY
CC   CHARGED DOMAINS OF PRERIBOSOMAL PARTICLES (EXPORT) OR OF RIBOSOMAL
CC   PROTEINS (IMPORT). BINDS NUCLEAR LOCALIZATION SEQUENCES; THE
CC   BINDING TO SUCH SEQUENCES IS DEPENDENT ON PHOSPHORYLATION. THE
CC   STATE OF PHOSPHORYLATION MAY REPRESENT A MEANS OF REGULATING THE
CC   PROTEIN'S AFFINITY FOR NLS-CONTAINING PROTEINS AND THEREBY ITS
CC   ABILITY TO FUNCTION IN NUCLEOCYTOPLASMIC TRANSPORT.
-!- SUBCELLULAR LOCATION: SHUTTLES ON CURVILINEAR TRACKS BETWEEN
CC   NUCLEOLUS AND CYTOPLASM. THESE TRACKS EXTEND FROM THE DENSE
CC   FIBRILLAR COMPONENT OF THE NUCLEOLUS ACROSS THE NUCLEOPLASM TO
CC   A LIMITED NUMBER OF NUCLEAR PORE COMPLEXES.
-!- PTM: THIS PROTEIN UNDERGOES RAPID AND MASSIVE PHOSPHORYLATION AND
CC   DEPHOSPHORYLATION ON CK-II AND PKC SITES. NOPP140 IS ONE OF THE
CC   MOST PHOSPHORYLATED PROTEINS IN THE CELL.
CC   -----------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------
DR   EMBL; M94287; AAA41718.1; -.
DR   EMBL; M94288; AAA41719.1; -.
KW   Nuclear protein; Phosphorylation; Repeat; Chaperone; Transport.
FT   DOMAIN       84    570       11 X 12 AA APPROXIMATE PREATS OF AN
FT                                ACIDIC SERINE CLUSTER.
FT   REPEAT       84     95       ACIDIC SERINE CLUSTER 1.
FT   REPEAT      127    138       ACIDIC SERINE CLUSTER 2.
FT   REPEAT      170    181       ACIDIC SERINE CLUSTER 3.
FT   REPEAT      231    242       ACIDIC SERINE CLUSTER 4.
FT   REPEAT      274    285       ACIDIC SERINE CLUSTER 5.
FT   REPEAT      335    346       ACIDIC SERINE CLUSTER 6.
FT   REPEAT      373    384       ACIDIC SERINE CLUSTER 7.
FT   REPEAT      434    445       ACIDIC SERINE CLUSTER 8.
FT   REPEAT      479    490       ACIDIC SERINE CLUSTER 9.
FT   REPEAT      524    535       ACIDIC SERINE CLUSTER 10.
FT   REPEAT      559    570       ACIDIC SERINE CLUSTER 11.
FT   VARIANT     150    150       MISSING (IN NOPP140B).
FT   MOD_RES     150    150       PHOSPHORYLATION (BY CK2).
FT   DOMAIN      126    131       POLY-SER.
FT   DOMAIN      136    140       POLY-GLU.
FT   DOMAIN      141    146       POLY-LYS.
FT   DOMAIN      226    236       POLY-SER.
FT   DOMAIN      274    277       POLY-SER.
FT   DOMAIN      283    287       POLY-GLU.
FT   DOMAIN      432    435       POLY-SER.
FT   DOMAIN      439    442       POLY-SER.
FT   DOMAIN      478    487       POLY-SER.
FT   DOMAIN      521    528       POLY-SER.
FT   DOMAIN      566    572       POLY-GLU.
SQ   SEQUENCE   704 AA;  73562 MW;  14DF1BF2DE483EA3 CRC64;


Query Match    7.6%;  Score 175.5;  DB 1;  Length 704;
Best Local Similarity   21.7%;  Pred. No. 0.049;
Matches   99;  Conservative   60;  Mismatches 183;  Indels 115;  Gaps 18;

Qy   44  KESPLQTPTPEDGSEEEPGSETSDAKSPTTAEDVTAPLVDEGAPGKQAAAQPH-----TEIP 98
         |:||:||::|||:: :||||::::|| | |:::| ||||||||  ||  |  | : |
Db   76  KRAKKETSSSDSSED-SSEEEDKAQVPTQK------AAAPAKRASLPQHAGRAAAKAS 126

Qy   99  EGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDKKAKGADGRKIATPRGAA 158
         |:::|:|::  :|     :|  |    :|| |  ||:|:||||||||::||| |||||
Db  127  ESSSSEESSEEEE----EKDKRKKPVQQRAVRPQAKAVRPPPKRAESSESESD-SSSEDEA 182

Qy  159  PPGQKGQANATRIPAKT-------PPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTP 213
         | :|| :| ||:|| ||       |:| || | ||| | |:|:|  :||| || |||:: |
Db  183  PQTQKPKRAAATAAKAPTKAQTKAPAKPGPPAKAQPRAANGRAGSSSSSSSSSDDSEEE 242

Qy  214  SLPTPTPRE--PKKVAVVRTPPK-----------------------SPSSAKSRLQTAP-------V 248
         |:   || :  |||:| ||| |                         ||:||  :|  |       |
Db  243  KRAAAPLRKTAPKKQVVAKAPVKVTAAPTQKSSSSEDSSSEEEEEDCKRPMKKKAGPYSSV 302

Qy  249  PMPDLKNVKSKIG----------------STENLKHQPG------GGKV 275
         |  ::   |||||                :||||:||||      |||:
Db  303  PPPSVSLSKKSVGAQSPKRAAAQTQPADSSADSSEEDSDSSSEEERKTPAKTVVSRKTPAKP 362

Qy  276  QIINKKLDLSNVQSKCCGSKDNIKHVPGGGSVQIVYKPVDLSK-------VTSKCGSLGNI 328
         : :|||  | :: || |  :|   |    | :| | | | | |       |:||| || |:
Db  363  APVKKAAESSDSSDSDSSDSSED-------------EAPAKPVSATKSPLSKPAVTPKPPAKAV 412

Qy  329  --HHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKT 386
           |::|  | ||:|||||:|||||||||||||||||||||||||:|||:||| ||:||:|
Db  413  ATPKQPAGSGQKPQSRRADSSSSSEEESSSSEEEAT------KKSVTPKA--RVTAKAAP 464

Qy  387  DHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSP 423
         : |||| |||| |||:||:  | |:||:|||||||:|
Db  465  SLPAK---QAPRAGGDSS----SDSESSSSEEEKKTP 494


RESULT 14
NFM_CHICK
ID   NFM_CHICK    STANDARD;    PRT;    857 AA.
AC   P16053;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   NEUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN)
DE   (NF-M).
GN   NEFM.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90174973.
RA   Zopf D., Dineva B., Betz H., Gundelfinger E.D.;
RT   "Isolation of the chicken middle-molecular weight neurofilament
RT   (NF-M) gene and characterization of its promoter.";
RL   Nucleic Acids Res. 18:521-529(1990).
RN   [2]
RP   SEQUENCE OF 259-857 FROM N.A.
RX   MEDLINE; 88112814.
RA   Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D., Betz H.;
RT   "Identification of gene products expressed in the developing chick
RT   visual system: characterization of a middle-molecular-weight
RT   neurofilament cDNA.";
RL   Genes Dev. 1:699-708(1987).
CC   -!- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
```

CC　　　AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
CC　-!- PTM: PHOSPHORYLATED ON A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS
CC　　　PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
CC　　　THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF
CC　　　INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
CC　　　OF AXONAL CALIBER.
CC　-!- PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
CC　　　OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
CC　　　LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
CC　　　COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
CC　-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CC
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DR　EMBL; X17102; CAA34958.1; -.
DR　EMBL; X05558; CAA29073.1; -.
DR　PIR; A27040; A27040.
DR　PIR; S08061; S08061.
DR　PIR; S15762; S15762.
DR　PFAM; PF00038; filament; 1.
DR　PROSITE; PS00226; IF; 1.
KW　Intermediate filament; IF; 1.
KW　Phosphorylation; Glycoprotein.
FT　INIT_MET　　0　　0
FT　DOMAIN　　1　98　HEAD.
FT　DOMAIN　　99　406　ROD.
FT　DOMAIN　　407　857　TAIL.
FT　DOMAIN　　99　130　COIL 1A.
FT　DOMAIN　　131　143　LINKER 1.
FT　DOMAIN　　144　242　COIL 1B.
FT　DOMAIN　　243　259　LINKER 12.
FT　DOMAIN　　260　281　COIL 2A.
FT　DOMAIN　　282　285　LINKER 2.
FT　DOMAIN　　286　406　COIL 2B.
FT　DOMAIN　　286　406　COIL 2B.
FT　CARBOHYD　46　46　O-LINKED (GLCNAC).
FT　CARBOHYD　426　426　O-LINKED (GLCNAC) (BY SIMILARITY).
FT　CARBOHYD　546　546　O-LINKED (GLCNAC) (BY SIMILARITY).
FT　CONFLICT　546　546　G -> R (IN REF. 2).
SQ　SEQUENCE　857 AA; 95704 MW; 4E2E0FC6AC64778B CRC64;

Query Match　　　20.0%; Score 175.5; DB 1; Length 857;
Best Local Similarity　　20.0%; Pred. No. 0.06; Mismatches 153; Indels 109; Gaps 14;
Matches　　81; Conservative　62;

Qy　　6　QEFEVMEDHAGQDTYGLGDRKDQGGYTMHQEGDTDAGLKESPLQTPIEDGSEEPGSEFSD　65
　　　　　:|.||||.| |.|| ||.|:|:|.|| || |||.||. :||.|
Db　510　EEEEKEEEEAEEEEAAKSDAAEEGGSKKEEIEEKEEGEEEAEEEEAEAKGKAEEEAGAKVEK　569

Qy　66　AKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQA　125
　　　　:||.:| | |||| ||| |.|.|.||..||| ||:|
Db　570　VKSPPAK------------SPPKSPPKSPVTE---------------------QA　591

Qy　126　RMYSKSKDGTGTGSDDKKAKGAD-----------GKTKIATPRGAPPGQKGQGANATRI　171
　　　　:|| ||
Db　592　KAVQKAAAAEVGKDQKAEKAAEKAAAEKAAASPEKPATPKVTSPEKPATPEKPTPEKAIT　651

Qy　172　PAK--TPPAPKTP--------PSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPP--　219
　　　　|.|| |:| |:| | || |||| |
Db　652　PEKVRSPEKPTTPEKVVSPEKPASPEKPRTPEKP--ASPEKPATP-EKPRTPEKPATPEK　708

Qy　220　TREPEKVAVRTPPKSPSPSSAKSRLQTPAVPMPDLKNVSKIGSTENLKHQPGGGKVQIIN　279
　　　　:|.|||. :|.|:|
Db　709　PRSPEK------PSSPLKDERAVVEESITVTKVTALEVEVSKEARKEDIAVNGEVEE　761

Qy　280　KKLDLSNYQSKCGSSKDNIKHVPGGGSVGIVYKPVDLSKVTSKCGSLGNIHHKPGGGVEV　339
　　　　||:||. |:|||
Db　762　KKDEAKEKEAEEEKG----------------------VVTNGLDVSPVDEK------　797

Qy　340　--KSEKLDFK--DRVQSKIGSLDNIHVPGGGNKKIETHKLTFRE　380
　　　　:|:|| :|| .| .| :| :|| :||
Db　798　TKRAEKITSEGGDSTTIVITKSVTVT-------QKVEEHEESFEE　835

RESULT 15
ICPO_HSV2H
ID　ICPO_HSV2H　　　STANDARD;　　PRT;　825 AA.
AC　P28284;
DT　01-DEC-1992 (Rel. 24, Created)
DT　01-DEC-1992 (Rel. 24, Last sequence update)
DT　15-JUL-1998 (Rel. 36, Last annotation update)
DE　TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
GN　RL2.
OS　Herpes simplex virus (type 2 / strain HG52).
OC　Viruses; dsDNA viruses; no RNA stage; Herpesviridae;
OC　Alphaherpesvirinae; Simplexvirus.
RN　[1]
RP　SEQUENCE FROM N.A.
RA　Dolan A.;
RL　Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RN　[2]
RP　SEQUENCE FROM N.A.
RA　McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
RT　"Comparative sequence analysis of the long repeat regions and
RT　adjoining parts of the long unique regions in the genomes of herpes
RT　simplex viruses types 1 and 2.";
RL　J. Gen. Virol. 72:3057-3075(1991).
CC　-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC　-!- SIMILARITY: TO OTHER HERPESVIRUSES ICP0 PROTEIN.
CC
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DR　EMBL; D10471; BAA23427.1; -.
DR　EMBL; Z86099; CAB06760.1; -.
DR　PIR; JQ1501; EDBEXD.
DR　PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
DR　PFAM; PF00097; zf-C3HC4; 1.
KW　Transcription regulation; Trans-acting factor; Activator; Zinc-finger;
KW　DNA-binding.
FT　DOMAIN　120　123　POLY-GLY.
FT　ZN_FING　126　152　C3HC4-TYPE.
FT　DOMAIN　266　271　POLY-GLY.
FT　DOMAIN　292　295　POLY-SER.
FT　DOMAIN　342　345　POLY-ALA.
FT　DOMAIN　386　389　POLY-SER.
FT　DOMAIN　395　400　POLY-GLY.
FT　DOMAIN　425　428　POLY-ALA.
FT　DOMAIN　590　603　POLY-SER.
FT　DOMAIN　595　618　POLY-SER.
FT　DOMAIN　610　627　POLY-SER.
SQ　SEQUENCE　825 AA; 81986 MW; 5CEB15858553A274 CRC64;

Query Match　　　24.1%; Score 163.5; DB 1; Length 825;
Best Local Similarity　　24.1%; Pred. No. 0.22; Mismatches 120; Indels 139; Gaps 18;
Matches　　92; Conservative　31;

Qy　　2　AEPEQEFEVMEDHAGQDTYGLGDRKDQGGYTMHQEGDTD----AGLKES--PLQTPTE　53
　　　　|:||| |:|||| ||| |.||||
Db　47　SEEETEVGISDDLHRD------------STSEAGSTDTEMFEAGLMDAATPPARPPAE　93

Qy　54　-DGSEEPGSETSDAKSPTAE-------------DVTAPLVDEGAPGKQAAAQP------　93
　　　　:|:::| |:||
Db　94　RQGSPTPADAQGSCGGGPVGEEEAEEAAGGGDVCAVCTDEIAPPLRCQSFPCLHFCIPCM　153

```
Qy    94  HTEIPEGTTAEEAG--------IGDTPS---------------LEDEAA-----------  119
              | :|    |||                           |   |||
Db   154  KTWIPLRNTCPLCNTPVAYLIVGVTASGSFSTIPIVNDPRTRVEAEAAVRAGTAVDFIWT  213

Qy   120  ---------GHVTQARMVSKSKDGTGSDDKRAKGADGKTKIATPRGAAPPGQKGQA      166
                       | :|  :|  |:||:                      ||    |
Db   214  GNPRTAPRSLSLGGHTVRA--LSPTPPWPGTDDEDDDLADVDYPPAPR-RAPRRGGGGA   270

Qy   167  NATR---IPAKTPPAPKTPP----SSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLP---  216
              |||    | || | |:|       | :| |   |    |   ||:   |||
Db   271  GATRGTSQPAATRPAPPGAPRSSSSGGAPLRAGVGSG--SGGGPAVAAVVPRVASLPPAA  328

Qy   217  --------------TPPTREPK-----KVAVRTPPKSPSSAKSRLQTAPVPMP         251
                            ||| ::|:         |  :  :
Db   329  GGGRAQAARVGEDAAAAEGRTPPARQPRAAQEPPIVISDSPPPSP-----RRPAGPGPLS  383

Qy   252  DLKNVKSKIGSTENLKHQPGG                                        273
              :  :   ::        ||||
Db   384  FVSSSSAQVSS------GPGGG                                       399
```

Search completed: September 28, 2000, 20:03:59
Job time: 287 sec

OM protein - protein search, using sw model

GenCore version 4.5
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Run on: September 28, 2000, 19:58:24 ; Search time 49.63 Seconds
(without alignments)
616.086 Million cell updates/sec

Title: US-09-142-613-1
Perfect score: 2295
Sequence: 1 MAEPRQEFEVMEDHAGQDTY.........SPQLATLADEVSASLAKQGL 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues
Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_12:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
11: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
1	1993.5	86.9	430	11	Q60684	Q60684 mus musculu
2	1878	81.8	402	6	Q60828	O60828 capra hircu
3	1861.5	81.8	686	11	Q63567	Q63567 rattus norv
4	1710.5	74.5	374	11	Q63677	Q63677 rattus norv
5	1698.5	74.5	372	11	Q60685	Q60685 mus musculu
6	1659.5	72.3	416	11	Q28187	Q28187 bos taurus
7	1587.5	69.2	350	11	Q60686	Q60686 mus musculu
8	1524	66.4	369	6	Q28185	Q28185 bos taurus
9	1415	61.7	347	6	Q28188	Q28188 bos taurus
10	1410	61.4	365	6	Q28186	Q28186 bos taurus
11	1337.5	58.3	338	6	Q28190	Q28190 bos taurus
12	1228.5	53.5	316	6	Q28189	Q28189 bos taurus
13	717.5	31.3	1825	11	Q64715	Q64715 rattus norv
14	714	31.1	1828	11	Q63724	Q63724 rattus norv
15	710	30.9	323	6	Q28869	Q28869 bos taurus
16	690.5	30.1	198	11	P97749	P97749 rattus norv
17	626	27.3	124	11	Q62286	Q62286 mus musculu
18	546	23.8	381	11	Q64710	Q64710 rattus norv
19	545	23.7	1152	4	Q13082	Q13082 homo sapien
20	481	21.0	125	4	Q16296	Q16296 homo sapien
21	403.5	17.6	1224	13	Q9Y190	Q9Y190 xenopus lae
22	364.5	15.9	431	5	Q17364	Q17364 caenorhabdi
23	364.5	15.9	453	5	O02592	O02592 caenorhabdi
24	347	15.1	113	13	O12967	O12967 fugu rubrip
25	329.5	14.4	413	5	P90973	P90973 caenorhabdi
26	328	14.3	436	5	Q17365	Q17365 caenorhabdi
27	278	12.1	242	5	Q20350	Q20350 caenorhabdi
28	246.5	10.7	928	13	Q98906	Q98906 gallus gall
29	193.5	8.4	1560	11	O88323	O88323 mus musculu
30	192	8.4	2187	11	P70670	P70670 mus musculu
31	184.5	8.0	1211	11	O35233	O35233 mus musculu
32	183.5	8.0	1566	4	O50279	O50279 mycoplasma
33	181.5	7.9	1581	4	O43810	O43810 homo sapien
34	181.5	7.9	3507	5	O75447	O75447 homo sapien
35	179	7.8	3507	5	Q23587	Q23587 caenorhabdi
36	178	7.8	971	5	Q9XV54	Q9XV54 caenorhabdi
37	177.5	7.7	487	13	O73793	O73793 serinus can
38	176	7.7	990	13	Q91803	Q91803 xenopus lae
39	175.5	7.6	2441	11	O96124	O96124 plasmodium
40	173	7.5	903	5	O77788	O77788 bos taurus
41	173	7.5	903	5	Q17917	Q17917 caenorhabdi
42	172.5	7.5	455	6	O04961	O04961 plasmodium
43	172.5	7.5	880	5	O17338	O17338 caenorhabdi
44	172.5	7.5	930	5	O17339	O17339 caenorhabdi
45	172	7.5	744	2	O69995	O69995 streptomyce

ALIGNMENTS

RESULT 1
Q60684

```
ID   Q60684      PRELIMINARY;      PRT;   430 AA.
AC   Q60684;
DT   01-NOV-1996 (TREMBLrel. 01, Created)
DT   01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TREMBLrel. 01, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 23.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HIM OF1 SPF; TISSUE=LIVER;
RA   KENNER L., EFERL R., ZATLOUKAL K., HOEFLER G., DENK H.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U12914; AAA58343.1; -.
DR   PROSITE; PS00229; TAU_MAP; 4.
DR   PFAM; PF00418; tubulin-binding; 4.
KW   Microtubules; Repeat.
SQ   SEQUENCE   430 AA;  44893 MW;  FD52F55A CRC32;

Query Match            86.9%;  Score 1993.5;  DB 11;  Length 430;
Best Local Similarity  87.9%;  Pred. No. 6.5e-119;
Matches  391;  Conservative  16;  Mismatches  19;  Indels  19;  Gaps  4;

Qy    1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTM--HQEGDTDAGLKESPLQTPTEDGSEE 58
          |:|:||||: |||||||                   |:|| |||| ||||:||  |:||
Db    1 MADPRQEFDTMEDHAGD--------------------YILLQDQGDMDHGLIKESPPQPPADDGAEE 47

Qy   59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
         ||||||||||||||||||||||||| ||:||||||||||||||:||||||||||| | ||
Db   48 PGSETSDAKSTPTAEDVTAPLVDERAPDKQAAAQPHTEIPEGITAEEAGIGDTPNQEDQA 107

Qy  119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQKGQANATRIPAKTP 176
         ||||||||:|   |:  :|:||||||||||| |||||||||||:  ||| :|||||||| |
Db  108 AGHVTQARVA--SKDRGNDEKKAKGADGKTGAKIATPRGAASPAQKGTSNATRIPAKTT 165

Qy  177 PAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 236
         |:||||| |||||||:|||||||||||||||||||||||||||||||||||||||||||
Db  166 PSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 225
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Qy    237  SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 296
           ::|:||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db    226  SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 285

Qy    297  IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    286  IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 345

Qy    357  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 405

Qy    417  IDMVDSPQLATLADEVSASLAKQGL 441
           ||||||||||||||||||||||||
Db    406  IDMVDSPQLATLADEVSASLAKQGL 430
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RESULT  2

ID   Q02828;                    PRELIMINARY;    PRT;    402 AA.
AC   Q02828;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN TAU.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Caprinae; Capra.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN CORTEX;
RX   MEDLINE; 97012131.
RA   NELSON P.T., STEFANSSON K., GULCHER J., SAPER C.B.;
RT   "Molecular evolution of tau protein: implications for Alzheimer's
RT   disease.";
RL   J. Neurochem. 67:1622-1632(1996).
CC   -!- FUNCTION: HEAT STABLE PROTEIN WHICH PROMOTES MICROTUBULE ASSEMBLY
CC       AND STABILITY, AND MIGHT BE INVOLVED IN THE ESTABLISHMENT AND
CC       MAINTENANCE OF NEURONAL POLARITY. BINDS AND STABILIZES AXONAL
CC       MICROTUBULES WHICH IS IMPORTANT FOR MAINTAINING AXONAL TRANSPORT
CC       AND DEFINING THE POLARITY OF A NEURON. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST TWO DIFFERENT ISOFORMS; TAU-A AND
CC       TAU-B (SHOWN HERE); OF TAU ARE PRODUCED BY DEVELOPMENTALLY AND
CC       TISSUE-SPECIFICALLY CONTROLLED ALTERNATIVE SPLICING. THEY DIFFER
CC       FROM EACH OTHER BY THE PRESENCE OR ABSENCE OF TWO EXONS/INSERTS,
CC       ONE CONTAINING THE ADDITIONAL TAU/MAP REPEAT. SHORT FORMS ALLOW
CC       PLASTICITY OF THE CYTOSKELETON WHEREAS LONGER FORMS MAY
CC       PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN. TYPE I TAU CONTAINS
CC       THREE REPEATS WHILE TYPE II TAU CONTAINS FOUR REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES IN
CC       (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN MITOSIS), AND AT
CC       SERINE RESIDUES IN K-X-G-S MOTIFS BY MAP/MICROTUBULE AFFINITY-
CC       REGULATING KINASE (MARK).
CC   -!- SIMILARITY: CONTAINS 4 OR 5 TAU/MAP REPEATS, FROM WHICH ONE IS
CC       APPROXIMATE, DEPENDING ON THE ISOFORM.
DR   EMBL; S83347; AAB50785.1; -.
DR   PROSITE; PS00229; TAU_MAP; 4.
PFAM; PF00418; tubulin-binding; 4.
KW   Microtubules; Repeat; Alternative splicing; Cytoskeleton; Acetylation;
KW   Phosphorylation.
FT   INIT_MET      0      0
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   MOD_RES       0      0       BY SIMILARITY.
FT   REPEAT      213    243       TAU/MAP MOTIF.
FT   REPEAT      244    274       TAU/MAP MOTIF.
FT   REPEAT      275    305       TAU/MAP MOTIF.
FT   REPEAT      306    337       TAU/MAP MOTIF.
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FT   DISULFID    252    283       BY SIMILARITY.
FT   MOD_RES     223    223       PHOSPHORYLATION (BY MARK) (POTENTIAL).
FT   MOD_RES     254    254       PHOSPHORYLATION (BY MARK) (POTENTIAL).
FT   MOD_RES     285    285       PHOSPHORYLATION (BY MARK) (POTENTIAL).
FT   MOD_RES     317    317       PHOSPHORYLATION (BY MARK) (POTENTIAL).
FT   VARSPLIC     33     33       PHOSPHORYLATION (BY MARK).
FT   VARSPLIC    236    236       MISSING (IN TAU-A).
FT   VARSPLIC     61     61       MISSING (IN TAU-A).
FT   VARSPLIC    266    266       MISSING (IN TAU-A).
SQ   SEQUENCE    402 AA;    41716 MW;    FC1E79AB CRC32;

Query Match      81.8%;   Score 1878;   DB 6;   Length 402;
Best Local Similarity   84.4%;   Pred. No. 1.2e-111;
Matches  374;   Conservative   8;   Mismatches   17;   Indels  44;   Gaps   4;

Qy      2  AEPRQEFEVMEDHAGQDTYGLGDRRDQGGYTMH-OEGDTDAGLKESPLQTPTEDGSEEPG   60
           |||||||||||||||||||||||||||||||| |||::|||||||||||||||||||||
Db      1  AEPRQEFDVMEDHA------------------------QGDYTLQDHEGDMEPGLKESPLQTPADGGSEEPG   48

Qy     61  SETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAG  120
           |||||||||||:||||
Db     49  SETSDAKSTPTAE------------------------AEEAGIGDTSNLEDQAAG   79

Qy    121  HVTQARMVSRSKDGTGSDDKKAKGADGK--TKIATPRGAAPPGQKGQANATRIPAKTPA  178
           ||||||||||||||||| ||||||| || |||:||||||||:|||||||||||||||||:|
Db     80  HVTQAMVSRSKDGTGPDDKKAKGADGKPGTKIATPRGAAPPGQKGQANATRIPAKTPT  139

Qy    179  PKTPPSSGEPPKSGDRSGYSSPSPGSPGTPGSRSRTPSLPTPPTRREPKKVAVVRTPPKSPSS  238
           ||||:|||||||||||||||||||||||||||||||:|||||||||||||||||||:||
Db    140  PKTSPGTGESGKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSA  199

Qy    239  AKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK  298
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    200  AKSRLQAAPGPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIK  259

Qy    299  HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD  358
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    260  HVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLD  319

Qy    359  NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID  418
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    320  NITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSID  379

Qy    419  MVDSPQLATLADEVSASLAKQGL  441
           |||||||||||||||||||||||
Db    380  MVDSPQLATLADEVSASLAKQGL  402
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RESULT  3

ID   O63567;                    PRELIMINARY;    PRT;    686 AA.
AC   O63567;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BIG TAU.
GN   TAU.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92179305.
RA   GOEDERT M., SPILLANTINI M.G., CROWTHER R.A.;
RT   "Cloning of a big tau microtubule-associated protein characteristic of
RT   the peripheral nervous system.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1983-1987(1992).
DR   EMBL; M84156; AAA42204.1; -.
DR   PROSITE; PS00229; TAU_MAP; 4.
PFAM; PF00418; tubulin-binding; 4.
KW   Microtubules; Repeat.
SQ   SEQUENCE    686 AA;    71774 MW;    70992021 CRC32;
```

RESULT 4

```
Qy   Query Match
     Best Local Similarity   81.1%;   Score 1861.5;  DB 11;  Length 686;
     Matches 391;  Conservative 15;  Mismatches 22;  Indels 271;  Gaps 4;

Qy      1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTM--HQEGDTDAGLKESPLQTPTEDGSEE 58
          ||||||||:|||| |||||
Db      1 MAEPRQEFDTMEDQAGD-------------------------------------------- 1

Qy     59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
          |||||:||||||||||||||||:||| ||||||||||:||||| ||:||||::|:|
Db     48 PGSETSDAKSTPTAEDVTAPLVEERAPDKQATAQSHTEIPEGTTAEEAGIGDTPNMEDQA 107

Qy    119 AGHVTQ------------------------------------------------------ 124
          ||||||
Db    108 AGHVTQEPQKVEIFSQSLIVEPGRREGQAPDSGISDWTHQQVPSMSGAPLPPQGLREATH 167

Qy    125 ------------------------------------------------------------ 124
Db    168 QPLGTRPEDVERSHPASELLMQESPQKEAWGKDRLGSSEEEVDEDITMDESSQESPPSQAS 227

Qy    125 ------------------------------------------------------------ 124
Db    228 LAPGTATPQARSVSASGVSGETTSIPGFPAEGSIPLPADFFSKVSAETQASPPEGPGTGP 287

Qy    125 ------------------ARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQ 162
                            |:|:||||||||::|||::|:| ||:||||
Db    288 SEEGHEAAPETFHVEIKASAPKEQDLEGATVGAPAEEQKARGPSVGKGTKEASLLEPT 347

Qy    163 KGQANATRIPAKTPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTRE 222
          |:|||:||||||||| |||||:|||||||||||:||||||||||||||:||||||| |
Db    348 DKQPAAGLPGPGPVSRVPQLKARVAGVSKDRTGNDEKKAKGADGKTGAKIATPRGAATPGQ 407

Qy    223 PKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKL 282
          |||:|||||||||:|:||||||||||||||||:|||||||||||||||||||||||:
Db    408 KGTSNATRIPAKTTPSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTRE 467

Qy    283 DLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSE 342
          ||||||||||:|||:||||||||||||||:||||:|||||||||||||||||||||||
Db    468 PKKVAVVRTPPKSPSASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKL 527

Qy    343 KLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGD 402
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    528 DLSNVQSKCGSKDNIKHVPGGGSVIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSE 587

Qy    403 TSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL 441
          |||||||||||||||||||||||||||||||||||||||
Db    648 TSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL 686
```

RESULT 5

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Qy   Query Match
     Best Local Similarity   74.5%;   Score 1710.5;  DB 11;  Length 374;
     Matches 342;  Conservative 14;  Mismatches 14;  Indels 75;  Gaps 4;

Qy      1 MAEPRQEFEVMEDHAGQDTYGLGDRKDQGGYTM--HQEGDTDAGLKESPLQTPTEDGSEE 58
          ||||||||:||||| |||||
Db      1 MAEPRQEFDTMEDQAGD-------------------------------------------- 1

Qy     59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
          |||||:||||||||||:||::|::|
Db     34 --------------------------------------------AEEAGIGDTPNMEDQA 49

Qy    119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQKGQANATRIPAKTP 176
          ||||||:|:|||||||||::|||::|:| ||:|||| |:||||:|:
Db     50 AGHVTQARVAGVSKDRTGNDEKKAKGADGKTGAKIATPRGAATPGQKGTSNATRIPAKTT 109

Qy    177 PAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 236
          |:|||||:||||||||||||:||||||||||||||||:||||||| |||:||||||||||
Db    110 PSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP 169

Qy    237 SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 296
          :|||||||||||||||||||:|||||||||||||||||||||||||:|||||||||:|||
Db    170 SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 229

Qy    297 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 356
          |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db    230 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 289

Qy    357 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    290 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 349

Qy    417 IDMVDSPQLATLADEVSASLAKQGL 441
          |||||||||||||||||||||||||
Db    350 IDMVDSPQLATLADEVSASLAKQGL 374
```

RESULT 4

ID   O63677   PRELIMINARY;   PRT;   374 AA.
AC   O63677;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   MICROTUBULE ASSOCIATED PROTEIN.
GN   TAU.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=BRAIN;
RX   MEDLINE; 94334997.
RA   SADOT E., MARX R., BARG J., BEHAR L., GINZBURG I.;
RT   "Complete sequence of 3'-untranslated region of Tau from rat central
RT   nervous system. Implications for mRNA heterogeneity.";
RL   J. Mol. Biol. 241:325-331(1994).
DR   EMBL; X79321; CAA55889.1; -.
DR   PROSITE; PS00229; TAU_MAP; -.
DR   PFAM; PF00418; tubulin-binding; 4.
KW   Microtubules; Repeat.
SQ   SEQUENCE   374 AA;   39117 MW;   79D40664 CRC32;

RESULT 5

ID   O60685   PRELIMINARY;   PRT;   372 AA.
AC   O60685;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HIM OF1 SPF; TISSUE=LIVER;
RA   KENER L., EFERL R., ZATLOUKAL K., HOEFLER G., DENK H.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U12915; AAA58344.1; -.
DR   PROSITE; PS00229; TAU_MAP; -.
DR   PFAM; PF00418; tubulin-binding; 4.
KW   Microtubules; Repeat.
SQ   SEQUENCE   372 AA;   38960 MW;   0CFE657B CRC32;

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RESULT 6
Q28187

ID   Q28187      PRELIMINARY;      PRT;    416 AA.
AC   Q28187;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TAU PROTEIN.
GN   TAU.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89261765.
RA   HIMMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT   "Tau consists of a set of proteins with repeated C-terminal
RT   microtubule-binding domains and variable N-terminal domains.";
RL   Mol. Cell. Biol. 9:1381-1388(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89261766.
RA   HIMMLER A.;
RT   "Structure of the bovine tau gene: alternatively spliced transcripts
RT   generate a protein family.";
RL   Mol. Cell. Biol. 9:1389-1396(1989).
DR   EMBL; M26178; AAA51601.1; -.
DR   EMBL; L34940; AAA51601.1; JOINED.
DR   EMBL; L34941; AAA51601.1; JOINED.
DR   EMBL; L34942; AAA51601.1; JOINED.
DR   EMBL; L34943; AAA51601.1; JOINED.
DR   EMBL; L34944; AAA51601.1; JOINED.
DR   EMBL; L34946; AAA51601.1; JOINED.
DR   EMBL; L34947; AAA51601.1; JOINED.
DR   EMBL; L34948; AAA51601.1; JOINED.
DR   EMBL; L34949; AAA51601.1; JOINED.
DR   EMBL; L34950; AAA51601.1; JOINED.
DR   EMBL; L34951; AAA51601.1; JOINED.
DR   PROSITE; PS00229; TAU_MAP; 4.
DR   PFAM; PF00418; tubulin-binding; 4.
KW   Microtubules; Repeat.

SQ   SEQUENCE   416 AA.;  42848 MW;  A5704F7 CRC32;

Query Match             72.3%;  Score 1659.5;  DB 6;  Length 416;
Best Local Similarity   84.3%;  Pred. No. 7.9e-98;
  Matches  328;  Conservative   9;  Mismatches  21;  Indels  31;  Gaps  4;

Qy     1 MADPRQEFDTMEDHAGD----------------YTLLQDQEGDMDHGLK------------- 33
Db     1 MADPRQEFDTMEDHAGD----------------YTLLQDQEGDMDHGLK------------- 33

Qy    34 ------------------------------AEEAGIGDTPNQEDQA 49
Db    34 ------------------------------AEEAGIGDTPNQEDQA 49

Qy    50 AGHVTQARVA--SKDRGNDEKKAKGADGKTCGKIATPRGAASPAQKGTSNATRIPAKTT 107
Db    50 AGHVTQARVA--SKDRGNDEKKAKGADGKTCGKIATPRGAASPAQKGTSNATRIPAKTT 107

Qy    59 PGSETSDAKSTPTAEDVTAPLVDEGAPCKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
Db    59 PGSETSDAKSTPTAEDVTAPLVDEGAPCKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118

Qy   108 PSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPKSP 167
Db   108 PSPKTPPGSGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPKSP 167

Qy   119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQKGQANATRIPAKTP 176
Db   119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQKGQANATRIPAKTP 176

Qy   168 SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 227
Db   168 SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 227

Qy   177 PAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPKSP 236
Db   177 PAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPKSP 236

Qy   228 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 287
Db   228 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 287

Qy   237 SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 296
Db   237 SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN 296

Qy   288 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 347
Db   288 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 347

Qy   297 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 356
Db   297 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS 356

Qy   348 IDMVDSPQLATLADEVSASLAKQGL 372
Db   348 IDMVDSPQLATLADEVSASLAKQGL 372

Qy   357 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416
Db   357 LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416

Qy   417 IDMVDSPQLATLADEVSASLAKQGL 441
Db   417 IDMVDSPQLATLADEVSASLAKQGL 441
```

```
RESULT 7
Q60686

ID   Q60686      PRELIMINARY;      PRT;    350 AA.
AC   Q60686;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HIM OF1 SPF; TISSUE=LIVER;
RA   KENNER L., EFERL R., ZATLOUKAL K., HOEFLER G., DENK H.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U12916; AAA58345.1; -.
DR   PROSITE; PS00229; TAU_MAP; 4.
DR   PFAM; PF00418; tubulin-binding; 4.
KW   Microtubules; Repeat.
SQ   SEQUENCE   350 AA.;  36740 MW;  9C54BC5E CRC32;

Query Match             69.2%;  Score 1587.5;  DB 11;  Length 350;
Best Local Similarity   72.4%;  Pred. No. 2.3e-93;
  Matches  322;  Conservative  12;  Mismatches  12;  Indels  99;  Gaps  5;

Qy     1 MAEPRQEFEVMEDHAGDTYGLGDRKDQGGYTM--EQEGDTDAGLKESPLQTPTEDGSEE 58
Db     1 MADPRQEFDVMEDHA----------------QGDTYLLQDQEGDMDHGLK---------- 33

Qy    59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEA 118
Db    34 --------------------------------YTLLQDQEGDMDHGLK-------------- 33

Qy   119 AGHVTQARMVSKSKDGTGSDDKKAKGADGKT--KIATPRGAAPPGQKGQANATRIPAKTP 176
```

RESULT 8

```
ID    Q28185
AC    Q28185;
DT    01-NOV-1996 (TrEMBLrel. 01, Created)
DT    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT    01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE    TAU PROTEIN.
GN    TAU.
OS    Bos taurus (Bovine).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC    Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC    Bovinae; Bos.
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE; 89261765.
RA    HIMMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT    "Tau consists of a set of proteins with repeated C-terminal
RT    microtubule-binding domains and variable N-terminal domains.";
RL    Mol. Cell. Biol. 9:1381-1388(1989).
RN    [2]
RP    SEQUENCE FROM N.A.
RX    MEDLINE; 89261766.
RA    HIMMLER A.;
RT    "Structure of the bovine tau gene: alternatively spliced transcripts
RT    generate a protein family.";
RL    Mol. Cell. Biol. 9:1389-1396(1989).
DR    EMBL; M26178; AAA51602.1; JOINED.
DR    EMBL; L34940; AAA51602.1; JOINED.
DR    EMBL; L34941; AAA51602.1; JOINED.
DR    EMBL; L34943; AAA51602.1; JOINED.
DR    EMBL; L34944; AAA51602.1; JOINED.
DR    EMBL; L34946; AAA51602.1; JOINED.
DR    EMBL; L34948; AAA51602.1; JOINED.
DR    EMBL; L34949; AAA51602.1; JOINED.
DR    EMBL; L34950; AAA51602.1; JOINED.
DR    EMBL; L34951; AAA51602.1; JOINED.
DR    PROSITE; PS00229; TAU_MAP; 4.
DR    PFAM; PF00418; tubulin-binding; 4.
KW    Microtubules; Repeat.
SQ    SEQUENCE  369 AA;  38212 MW;  948F16BD CRC32;
```

PRELIMINARY; PRT; 369 AA.

```
Query Match             66.4%;  Score 1524; DB 6;  Length 369;
Best Local Similarity   81.8%;
Matches  305;  Conservative  6;  Mismatches  16;  Indels  46;  Gaps  5;
```

```
Qy    34  ------ARVA--SKDN-DNDERKAKGADGKTKGARIATPRGAASPAQKGTSNATRIPAKTT  85
               ||||     ||||  |||||||||  |||||||||||||
Db     1  MAEPRQEFDVMEDHA-------------------------------------------  48

Qy   177  PAPKTPPSSGGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP  236
          |:||     |||   ||||  |||
Db    86  PSPKTPPSSGGEPPKSGERSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSP  145

Qy   237  SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN  296
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   146  SASKSRLQTAPVPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDN  205

Qy   297  IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS  356
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   206  IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGS  265

Qy   357  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS  416
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   266  LDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS  325

Qy   417  IDMVDSPQLATLADEVSASLAKQGL  441
          |||||||||||||||||||||||||
Db   326  IDMVDSPQLATLADEVSASLAKQGL  350
```

RESULT 9

```
ID    Q28188
AC    Q28188;
DT    01-NOV-1996 (TrEMBLrel. 01, Created)
DT    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT    01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE    TAU PROTEIN.
GN    TAU.
OS    Bos taurus (Bovine).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC    Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC    Bovinae; Bos.
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE; 89261765.
RA    HIMMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT    "Tau consists of a set of proteins with repeated C-terminal
RT    microtubule-binding domains and variable N-terminal domains.";
RL    Mol. Cell. Biol. 9:1381-1388(1989).
RN    [2]
RP    SEQUENCE FROM N.A.
RX    MEDLINE; 89261766.
RA    HIMMLER A.;
RT    "Structure of the bovine tau gene: alternatively spliced transcripts
RT    generate a protein family.";
RL    Mol. Cell. Biol. 9:1389-1396(1989).
DR    EMBL; M26178; AAA51605.1; -.
DR    EMBL; L34940; AAA51605.1; JOINED.
DR    EMBL; L34941; AAA51605.1; JOINED.
DR    EMBL; L34944; AAA51605.1; JOINED.
DR    EMBL; L34946; AAA51605.1; JOINED.
DR    EMBL; L34948; AAA51605.1; JOINED.
DR    EMBL; L34949; AAA51605.1; JOINED.
DR    EMBL; L34950; AAA51605.1; JOINED.
DR    EMBL; L34951; AAA51605.1; JOINED.
DR    PROSITE; PS00229; TAU_MAP; 4.
DR    PFAM; PF00418; tubulin-binding; 4.
KW    Microtubules; Repeat.
SQ    SEQUENCE  347 AA;  36016 MW;  00FD6406 CRC32;
```

PRELIMINARY; PRT; 347 AA.

```
Query Match             61.7%;  Score 1415; DB 6;  Length 347;
Best Local Similarity   76.7%;
Matches  286;  Conservative  4;  Mismatches  15;  Indels  68;  Gaps  5;
```

```
Qy    60  GSEISDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAA  119
          |||||||||||||||||||||||||||||      ||  |    ||| ||:||||
Db     1  GSEISDAKSTPTAE-----------------------------AEEAGIGDTSNLEDQAA  79

Qy   120  GHVTQARMVSKSKDGTGSDDKKAKGADGK--TKIATPRGAAPPGGKGQANATRIPAKTPP  177
          |||| |  || |||| ||||| ||||||   |||||||||||||||||||||||||||||
Db    80  GHVTQARMVSKGKDGTGPDDKKTKGADGRPGTKIATPRGAAPPGGKGQANATRIPAKTTP  139

Qy   178  APKTPPSSGGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPS  237
          ||| | ||||   ||||  |||                |||||||||||||||||||||||
Db   140  TPKTSP--GESGKGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPS  197

Qy   238  SAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNI  297
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198  AAKSRLQAAPGPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNI  257

Qy   298  KHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSL  357
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   258  KHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSL  317

Qy   358  DNITHVPGGGNKK  370
          |||||||||||||
Db   318  DNITHVPGGGNKK  330
```

```
Qy     1  MAEPRQEFFVMEDHAGQDTYGLGDRKDQGGYTMH-QEGDTDAGLKESPLQTPTEDGSEEP  59
                                       || |  ||  ||||  |||||||||:|||||||
Db     1  MAEPRQEFDVMEDHA-----------------QGDYTLQDQEGDMDPGLKESPLQTPADDGSEEP  48
```

```
RESULT 10

ID   Q28186
AC   Q28186;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TAU PROTEIN.
GN   TAU.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89261765.
RA   HIMMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT   "Tau consists of a set of proteins with repeated C-terminal
RT   microtubule-binding domains and variable N-terminal domains.";
RL   Mol. Cell. Biol. 9:1381-1388(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89261766.
RA   HIMMLER A.;
RT   "Structure of the bovine tau gene: alternatively spliced transcripts
RT   generate a protein family.";
RL   Mol. Cell. Biol. 9:1389-1396(1989).
DR   EMBL; M26178; AAA51604.1; JOINED.
DR   EMBL; L34940; AAA51604.1; JOINED.
DR   EMBL; L34941; AAA51604.1; JOINED.
DR   EMBL; L34944; AAA51604.1; JOINED.
DR   EMBL; L34946; AAA51604.1; JOINED.
DR   EMBL; L34947; AAA51604.1; JOINED.
DR   EMBL; L34948; AAA51604.1; JOINED.
DR   EMBL; L34949; AAA51604.1; JOINED.
DR   EMBL; L34950; AAA51604.1; JOINED.
DR   EMBL; L34951; AAA51604.1; JOINED.
DR   PROSITE; PS00229; TAU_MAP; 4.
DR   PFAM; PF00418; tubulin-binding; 4.
KW   Microtubules; repeat.
SQ   SEQUENCE 365 AA;  37923 MW;  08A4187E CRC32;
```

(Alignment block, Result 10)

```
Qy    1 MAEPRQEFDVMEDHA------------------QGDYTLQDQEGDMDPGLKESPLQTPADDGSEEP 48
        ||||||||||||||||                  || ||: |||||| |||||||||||||:|||||
Db    1 MAEPRQEFDVMEDHA------------------QGDYTLQDQEGDMDPGLKESPLQTPADDGSEEP 48

Qy   49 GSETSDAKSTPTAE---------------------------------------------------- 62
        |||||||||||||
Db   49 GSETSDAKSTPTAE---------------------------------------------------- 62

Qy   60 GSETSDAKSTPTAEDVTAPLVDEGAPGCKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAA 119
Db   60 GSETSDAKSTPTAEDVTAPLVDEGAPGCKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAA 119

Qy  120 GHVTQARMVSKSKDGTGSDDKKAKGADGK--TKIATPRGAAPPGQKGQANATRIPAKTPP 177
Db   63 ------ARMVSKGKDGTGPDDKKTKGADGKPGTKIATPRGAAPPGQKGQANATRIPAKTTP 117

Qy  178 APKTPPSSGEPPKSGDRSGYSSPGSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPS 237
Db  118 TPKTSP--GESGKSGDRSGYSSPGSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPS 175

Qy  238 SAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNI 297
Db  176 AAKSRLQAAPGPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNI 235

Qy  298 KHVPGGGSVQIVYKPVDLSKVTSKCCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSL 357
Db  236 KHVPGGGSVQIVYKPVDLSKVTSKCCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSL 295

Qy  358 DNITHVPGGGNKK 370
        |||||||||||||
Db  296 DNITHVPGGGNKK 308
```

Matches 286; Conservative 6; Mismatches 15; Indels 82; Gaps 5;

```
RESULT 11

ID   Q28190
AC   Q28190;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TAU PROTEIN.
GN   TAU.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89261765.
RA   HIMMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT   "Tau consists of a set of proteins with repeated C-terminal
RT   microtubule-binding domains and variable N-terminal domains.";
RL   Mol. Cell. Biol. 9:1381-1388(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89261766.
RA   HIMMLER A.;
RT   "Structure of the bovine tau gene: alternatively spliced transcripts
RT   generate a protein family.";
RL   Mol. Cell. Biol. 9:1389-1396(1989).
DR   EMBL; M26178; AAA51603.1; JOINED.
DR   EMBL; L34940; AAA51603.1; JOINED.
DR   EMBL; L34941; AAA51603.1; JOINED.
DR   EMBL; L34943; AAA51603.1; JOINED.
DR   EMBL; L34944; AAA51603.1; JOINED.
DR   EMBL; L34946; AAA51603.1; JOINED.
DR   EMBL; L34948; AAA51603.1; JOINED.
DR   EMBL; L34949; AAA51603.1; JOINED.
DR   EMBL; L34950; AAA51603.1; JOINED.
DR   EMBL; L34951; AAA51603.1; JOINED.
DR   PROSITE; PS00229; TAU_MAP; 3.
DR   PFAM; PF00418; Repeat.
KW   Microtubules; Repeat.
SQ   SEQUENCE 338 AA;  34965 MW;  F349F977 CRC32;
```

(Alignment block, Result 11)

```
Qy    1 MAEPRQEFFVMEDHAQGODTYGLGDRKDQGGTYMH-QEGDTDAGLKESPLQTPTEDGSEEP 59
Db    1 MAEPRQEFDVMEDHA--------QGDYTLQDQEGDMDPGLKESPLQTPADDGSEEP 48

Qy   60 GSETSDAKSTPTAEDVTAPLVDEGAPGCKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAA 119
Db   49 GSETSDAKSTPTAE---- 62

Qy  120 GHVTQARMVSKSKDGTGSDDKKAKGADGK--TKIATPRGAAPPGQKGQANATRIPAKTPP 177
Db   63 ------ARMVSKGKDGTGPDDKKTKGADGKPGTKIATPRGAAPPGQKGQANATRIPAKTTP 117

Qy  178 APKTPPSS--------------GEPPKSGDRSGYSSPGSPGSPGTPGSRSRTPSLPTPPTR 221
Db  118 TPKTSPATMQVQKKPPPAGAKSERGESGKSGDRSGYSSPGSPGSPGTPGSRSRTPSLPTPPTR 177

Qy  222 EPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKK 281
Db  178 EPKKVAVVRTPPKSPSAAKSRLQAAPGPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKK 237

Qy  282 LDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCCGSLGNIHHKPGGGQVEVKS 341
Db  238 LDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCCGSLGNIHHKPGGGQVEVKS 297

Qy  342 EKLDFKDRVQSKIGSLDNITHVPGGGNKK 370
        ||||||||||||||||||||||||||||
Db  298 EKLDFKDRVQSKIGSLDNITHVPGGGNKK 326
```

Query Match 61.4%; Score 1410; DB 6; Length 365;
Best Local Similarity 73.5%; Pred. No. 4e-82;

```
RESULT 12

Query Match         58.38;      Score 1337.5;  DB 6;  Length 338;
Best Local Similarity  73.5%;   Pred. No. 1.4e-77;
Matches  274;  Conservative   6;  Mismatches  16;  Indels  77;  Gaps   6;

Qy    1 MAEPRQEFEVMEDHAGDTYGLGDRKDQGGYTMH-QEGDTDAGLKESPLQTPTEDGSEEP 59
          ||||||||||:|||||||  |||: |||||||| :|:|| :|||||||||:|:|||||||
Db    1 MAEPRQEFDVMEDHA-------------QGDYTLQDQEGDMDPGLKESPLQTPADDGSEEP 48

Qy   60 GSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAA 119
          ||||||||||||||||                                |||||||||:||::||:
Db   49 GSETSDAKSTPTAE-----------------------AEEAGIGDTSNLEDQAA 79

Qy  120 GHVTQARMVSKSKDGTGSDDKKAKGADGK--TKIATPRGAAPPGQKGQANATRIPAKTPP 177
          |||||||| |||||| ||||:|||||:|||  |||||||||||||||||:||||||||||
Db   80 GHVTQARMVSKGKDGTGPDDKKTKGADGKPGTKIATPRGAAPPGQKGQANATRIPAKTTP 139

Qy  178 APKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPTPTREPKVAVVRTPPKSPS 237
          |||| || ||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db  140 TPKTSP--GESGKSGDRSGYSSPGSPGTPGSRSRTPSLPTPTPTREPKKVAVVRTPPKSPS 197

Qy  238 SAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNI 297
          :|||| | ||  ||||||||||||||||||||||||||||||  |||:|||||||||||
Db  198 AAKSRLQAAPGMPDLKNVKSKIGSTENLKHQPGGGK------------------------ 234

Qy  298 KHVPGGGSVQIYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSL 357
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  235 ------VQIYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSL 286

Qy  358 DNITHVPGGGNKK 370
          |||||||||||||
Db  287 DNITHVPGGGNKK 299

ID   Q28189         PRELIMINARY;      PRT;   316 AA.
AC   Q28189;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TAU PROTEIN.
GN   TAU.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89261765.
RA   HIMMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT   "Tau consists of a set of proteins with repeated C-terminal
RT   microtubule-binding domains and variable N-terminal domains.";
RL   Mol. Cell. Biol. 9:1381-1388(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89261766.
RA   HIMMLER A.;
RT   "Structure of the bovine tau gene: alternatively spliced transcripts
RT   generate a protein family.";
RL   Mol. Cell. Biol. 9:1389-1396(1989).
DR   EMBL; M26178; AAA51606.1; -.
DR   EMBL; L34940; AAA51606.1; JOINED.
DR   EMBL; L34941; AAA51606.1; JOINED.
DR   EMBL; L34944; AAA51606.1; JOINED.
DR   EMBL; L34946; AAA51606.1; JOINED.
DR   EMBL; L34948; AAA51606.1; JOINED.
DR   EMBL; L34950; AAA51606.1; JOINED.
DR   EMBL; L34951; AAA51606.1; JOINED.
DR   PFAM; PF00418; tubulin-binding; 3.
DR   PROSITE; PS00229; TAU_MAP; 3.
KW   Microtubules; Repeat.
SQ   SEQUENCE  316 AA;  32770 MW;  DEC3A429 CRC32;
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RESULT 13

Query Match         53.5%;      Score 1228.5;  DB 6;  Length 316;
Best Local Similarity  68.4%;   Pred. No. 1e-70;
Matches  255;  Conservative   4;  Mismatches  15;  Indels  99;  Gaps   6;

Qy    1 MAEPRQEFEVMEDHAGDTYGLGDRKDQGGYTMH-QEGDTDAGLKESPLQTPTEDGSEEP 59
          ||||||||||:|||||||  |||: |||||||| :|:|| :|||||||||:|:|||||||
Db    1 MAEPRQEFDVMEDHA-------------QGDYTLQDQEGDMDPGLKESPLQTPADDGSEEP 48

Qy   60 GSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAA 119
          ||||||||||||||||                                |||||||||
Db   49 GSETSDAKSTPTAE--------------------------------AEEAGIGDTSNLEDQAA 62

Qy  120 GHVTQARMVSKSKDGTGSDDKKAKGADGK--TKIATPRGAAPPGQKGQANATRIPAKTPP 177
          |||||||| |||||| |||||||:||||||  |||||||||||||||||||||||||||
Db   63 -----ARMVSKGKDGTGPDDKKTKGADGKPGTKIATPRGAAPPGQKGQANATRIPAKTTP 117

Qy  178 APKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPTPTREPKVAVVRTPPKSPS 237
          |||| || ||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db  118 TPKTSP--GESGKSGDRSGYSSPGSPGTPGSRSRTPSLPTPTPTREPKKVAVVRTPPKSPS 175

Qy  238 SAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNI 297
          :|||| | ||  |||||||||||||||||||||||||||||||  |||:||||||||||
Db  176 AAKSRLQAAPGMPDLKNVKSKIGSTENLKHQPGGGK------------------------ 212

Qy  298 KHVPGGGSVQIYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSL 357
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  213 ------VQIYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSL 264

Qy  358 DNITHVPGGGNKK 370
          |||||||||||||
Db  265 DNITHVPGGGNKK 277

ID   Q64715         PRELIMINARY;      PRT;  1825 AA.
AC   Q64715;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   MICROTUBULE ASSOCIATED PROTEIN 2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=BRAIN;
RA   DRESSE A.E.;
RC   STRAIN=WISTAR; TISSUE=BRAIN;
RL   Submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1802-1825 FROM N.A.
RC   STRAIN=WISTAR; TISSUE=BRAIN;
RX   MEDLINE; 89334524.
RA   MARECHAL D., DELAPORRE D., DRESSE A.;
RT   "Cloning and partial sequencing of a new rat brain specific cDNA.";
RL   Arch. Int. Physiol. Biochim. 96:231-236(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=BRAIN;
RX   MEDLINE; 95094034.
RA   FERHAT L., BEN-ARI Y., KIRESTCHATISKY M.;
RT   "Complete sequence of rat MAP2d, a novel MAP2 isoform.";
RL   C. R. Acad. Sci. III, Sci. Vie 317:304-309(1994).
DR   EMBL; X54100; CAA38031.1; -.
DR   EMBL; X74211; CAA52283.1; -.
DR   PFAM; PF00418; tubulin-binding; 2.
DR   PROSITE; PS00229; TAU_MAP; 2.
KW   Microtubules; Repeat.
FT   CONFLICT    151    151     Q -> VRLNKKIDFSKYQSRCGSKDNIKHSAGGN
FT                               (IN REF. 3).
FT   CONFLICT   1509   1509     MISSING (IN REF. 3).
FT   CONFLICT   1689   1689     Q -> VRILNKKIDFSKYQSRCGSKDNIKHSAGGN
FT                               (IN REF. 3).
SQ   SEQUENCE  1825 AA;  198565 MW;  AB7B2EAB CRC32;
```

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Query Match          31.3%;  Score 717.5;  DB 11;  Length 1825;
Best Local Similarity 39.2%;  Pred. No. 1.3e-37;
Matches 175;  Conservative 65;  Mismatches 109;  Indels 97;  Gaps 13;

Qy      44 KESPLQT-----------PIEDGSEEPGSETSDAKSTPTAEDVTAPL----VDEGAPGKQAA 90
              |  |  :::   :::  ||||:|:||:|:|:   |||  |  |      |||  |
Db    1429 KEKPFKTGRGRISTPERKVAKKEPSTVSRDEVRRKAVYKKAELAKKSEVQAHSPSRKLI 1488

Qy      91 AQPHTE--------IPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKRSKDGTGSDDKK 141
              |    |        ||  |  || | ||  |  |  |  | |  |  |  | |  |
Db    1489 LKPAIKYTRPTHLSCVKRKTTATSGGESAQAPSAFKQAKDKVT---------DGI 1533

Qy     142 AKGADGKTKIATPRGAAPP--GQKG--QANATRIPAKTPPAPKTPPSSGEPPKSGDRSGY 197
           :|::|||||||||||||||  || |  ||||||||||||||||||||||||||:||
Db    1534 TKSPEKRSSLPRPSSILPPRRGVSGDREENSFSLNSSISSARRTTRS--EPIRRAGKSGT 1591

Qy     198 SSPGSPG-----TPGS--------RSRTPSLPTPPT--REP---------KKVAVVRTPPKS 235
           ||:|||     ||||        ||||||||||||  |||         |||||:|||||
Db    1592 STPTPGSTAITPGGTPPPSYSSSRTPGTPSYPRPGTPKGILVPSERKVAIIRTPPKS 1651

Qy     236 NIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIG 295
           :|| || ::||| ||||||||:|||||||||:|||||||||:||||||||||:|||||:
Db    1652 PATPK-QLRLINQPLPDLKNVKSKIGSTDNIKYQPKGGQVQIVTKIDLSH------- 1701

Qy     296 PSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINRKLDLSNVQSKCGSKD 355
           ||:||||||||:||||||||:|||||||||:|||||||||:||||||||||:|||||||
Db    1702 VTSKCGSLKNIRIHRPGGGRVKIESVKLDFKEKAQAKVG 1739

Qy     356 SLDNITHVPGGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTG 415
           ||||:||||||| ||||||||||||||||:||||||:||||||||||||||||:|||||
Db    1740 SLDNAHHVPGGGNVKIDSQKLNFREHAKARVDHGAEIITQSPSRSSVASPRRLSNVSSSG 1799

Qy     416 SIDMVDSPQLATLADEVSASLAKQGL 441
           ||:||||:|||||||||:||||||||
Db    1800 SINLLESPQLATLAEDVTAALAKQGL 1825
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RESULT 14
Q63724
ID    Q63724;          PRELIMINARY;       PRT;  1828 AA.
AC    Q63724;
DT    01-NOV-1996 (TrEMBLrel. 01, Created)
DT    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT    01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE    MICROTUBULE-ASSOCIATED PROTEIN 2.
OS    Rattus norvegicus (Rat).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC    Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=RA25; TISSUE=BRAIN;
RA    MATUS A., DOLL T.;
RL    Submitted (MAY-1990) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; X53455; CAA37535.1; -.
DR    PROSITE; PS00229; TAU_MAP; 2.
DR    PFAM; PF00418; tubulin-binding; 3.
KW    Microtubule; Repeat.
SQ    SEQUENCE 1828 AA; 198982 MW; C754E9EA CRC32;
```

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Query Match          31.1%;  Score 714;  DB 11;  Length 1828;
Best Local Similarity 39.1%;  Pred. No. 2.1e-37;
Matches 174;  Conservative 66;  Mismatches 109;  Indels 96;  Gaps 13;

Qy      44 KESPLQT-----------PIEDGSEEPGSEISDAKSTPIAEDVTAPL----VDEGAPGKQAA 90
              |  |  :::   :::  ||||:|:||:|:|:   |||  |  |      |||  |
Db    1433 KEKPFKTGRGRISTPERKVAKKEPSTVSRDEVRRKAVYKKAELAKKSEVQAHSPSRKLI 1492

Qy      91 AQPHTE--------IPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKK 141
              |    |        ||  |  || | ||  |  |  |  | |  |  |  |  | |  |
Db    1493 LKPAIKYTRPTHLSCVKRKTTATSGESAQAPSAFKQAKDKVT---------DGI 1537
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Qy     142 AKGADGKTKIATPRGAAPP--GQKG--QANATRIPAKTPPAPKTPPSSGEPPKSGDRSGY 197
           :|::|||||||||||||||  || |  ||||||||||||||||||||||||||:||
Db    1538 TKSPEKRSSLPRPSSILPPRRGVSGDREENSFSLNSSISSARRTTRS--EPIRRAGKSGT 1595

Qy     198 SSPGSPG-----TPGS--------RSRTPSLPTPPT--REP---------KKVAVVRTPPKS 236
           ||:|||     ||||        ||||||||||||  |||         |||||:|||||
Db    1596 STPTPGSTAITPGGTPPPSYSSSRTPGTPSYPRPGTPKGILVPSERKVAIIRTPPKSP 1655

Qy     237 SSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINRKLDLSNVQSKCGSKDN 296
           ||:||||||||:||||||||:|||||||||:|||||||||:||||||||||:|||||||
Db    1656 ATPK-QLRLINQPLPDLKNVKSKIGSTDNIKYQPKGGQVQIVTKIDLSH------- 1704

Qy     297 IKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIG 356
           |||| || ::||| ||||||||:|||||||||:|||||||||:||||||||||:|||||
Db    1705 ---------VTSKCGSLKNIRIHRPGGGRVKIESVKLDFKEKAQAKVG 1743

Qy     357 LDNITHVPGGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGS 416
           |||:||||||| ||||||||||||||||:||||||:||||||||||||||||:||||||
Db    1744 LDNAHHVPGGGNVKIDSQKLNFREHAKARVDHGAEIITQSPSRSSVASPRRLSNVSSSG 1803

Qy     417 IDMVDSPQLATLADEVSASLAKQGL 441
           ||:||||:|||||||||:||||||||
Db    1804 INLLESPQLATLAEDVTAALAKQGL 1828
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RESULT 15
Q28869
ID    Q28869;          PRELIMINARY;       PRT;  323 AA.
AC    Q28869;
DT    01-NOV-1996 (TrEMBLrel. 01, Created)
DT    01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT    01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE    MICROTUBULE-ASSOCIATED PROTEIN 2 (MAP2) (FRAGMENT).
OS    Bos taurus (Bovine).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC    Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC    Bovinae; Bos.
RN    [1]
RP    SEQUENCE FROM N.A., AND CHARACTERIZATION OF TUBULIN REPEATS.
RC    TISSUE=BRAIN;
RX    MEDLINE; 95034751.
RA    COFFEY R.L., JOLY J.C., CAIN B.D., PURICH D.L.;
RT    "Exploring the microtubule-binding region of bovine microtubule-
RT    associated protein-2 (MAP-2): cDNA sequencing, bacterial expression,
RT    and site-directed mutagenesis.";
RL    Biochemistry 33:13199-13207(1994).
RN    [2]
RP    SEQUENCE OF 121-139.
RX    MEDLINE; 90037224.
RA    JOLY J.C., FLYNN G., PURICH D.L.;
RT    "The microtubule-binding fragment of microtubule-associated protein-2:
RT    location of the protease-accessible site and identification of an
RT    assembly-promoting peptide.";
RL    J. Cell Biol. 109:2289-2294(1989).
RN    [3]
RP    SEQUENCE OF 18-36 AND 227-258.
RX    MEDLINE; 92011652.
RA    DINGUS J., OBAR R.A., HYAMS J.S., GOEDERT M., VALLEE R.B.;
RT    "Use of a heat-stable microtubule-associated protein class-specific
RT    antibody to investigate the mechanism of microtubule binding.";
RL    J. Biol. Chem. 266:18854-18860(1991).
RN    [4]
RP    PHOSPHORYLATION.
RX    MEDLINE; 98026080.
RA    ITOH T.J., HISANAGA S., HOSOI T., KISHIMOTO T., HOTANI H.;
RT    "Phosphorylation states of microtubule-associated protein 2 (MAP2)
RT    determine the regulatory role of MAP2 in microtubule dynamics.";
RL    Biochemistry 36:12574-12582(1997).
-!- FUNCTION: HEAT STABLE PROTEIN WHICH PROMOTES MICROTUBULE ASSEMBLY
    AND STABILITY, AND MIGHT BE INVOLVED IN THE ESTABLISHMENT AND
    MAINTENANCE OF NEURONAL POLARITY. MAY PLAY A ROLE IN DENDRITIC
    POLARITY, OUTGROWTH, BRANCHING, PLASTICITY, SPACING, AND STABILITY
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CC    OF MICROTUBULES DURING DIFFERENT STAGES OF NEURONAL DEVELOPMENT.
CC    THE VARYING LENGTH OF THE PROJECTION ARM SERVES AS A SPACER
CC    BETWEEN MICROTUBULES.
CC -!- ALTERNATIVE PRODUCTS: AS IN OTHER MAMMALS, SEVERAL ISOFORMS
CC    INCLUDING ONE POSSESSING AN ADDITIONAL TAU/MAP REPEAT, MIGHT BE
CC    PRODUCED BY DEVELOPMENTALLY CONTROLLED ALTERNATIVE SPLICING.
CC -!- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN. THE SECOND REPEAT
CC    PLAYS A DOMINANT ROLE IN MICROTUBULE BINDING.
CC -!- PTM: PHOSPHORYLATION AT VARIOUS SITES IN THE N-TERMINAL BY A CAMP-
CC    DEPENDENT PROTEIN KINASE (PKA), IN THE PROLINE-RICH C-TERMINAL
CC    DOMAIN BY PROLINE-DIRECTED PROTEIN KINASES (CDC2, GSK3) AND OF
CC    SERINE RESIDUES IN K-X-G-S MOTIFS BY MAP/MICROTUBULE AFFINITY-
CC    REGULATING KINASE (MARK). IN VITRO PHOSPHORYLATION BY PKA AFFECTS
CC    THE MICROTUBULE-ASSEMBLING ACTIVITY, BY CDC2 AFFECTS BOTH THE
CC    MICROTUBULE-ASSEMBLING AND STABILIZING ACTIVITY OF MAP2.
CC    PHOSPHORYLATION BY MARK DECREASES TUBULIN-BINDING AND MICROTUBULES
CC    ASSEMBLY, ALLOWING THE REARRANGEMENT OF THE MICROTUBULE NETWORK.
CC -!- PTM: THE N-TERMINAL IS BLOCKED.
CC -!- MISCELLANEOUS: MUTAGENESIS EXPERIMENTS WERE DONE IN REF.1 IN WHICH
CC    THE FIRST AND THIRD REPEATS WERE MODIFIED TO RESEMBLE THE SECOND
CC    REPEAT WHICH LEAD TO SOMEWHAT HIGHER AFFINITY MICROTUBULE BINDING.
CC -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS, FROM WHICH ONE IS
CC    APPROXIMATE.
DR    EMBL; S74025; AAB32526.1; ALT_SEQ.
DR    PROSITE; PS00229; TAU_MAP; 2.
DR    PFAM; PF00418; tubulin-binding; 3.
KW    Microtubules; Repeat; Alternative splicing; Cytoskeleton;
KW    Phosphorylation.
FT    NON_TER        1      1
FT    REPEAT       156    187       TAU/MAP MOTIF.
FT    REPEAT       188    218       TAU/MAP MOTIF.
FT    REPEAT       219    250       TAU/MAP MOTIF.
FT    REPEAT       251    282       APPROXIMATE TAU/MAP MOTIF.
FT    MOD_RES       37     37       PHOSPHORYLATION (BY MARK) (BY
FT                                  SIMILARITY).
FT    MOD_RES      109    109       PHOSPHORYLATION (BY A PROLINE-DIRECTED
FT                                  KINASE) (BY SIMILARITY).
FT    MOD_RES      112    112       PHOSPHORYLATION (BY A PROLINE-DIRECTED
FT                                  KINASE) (BY SIMILARITY).
FT    MOD_RES      115    115       PHOSPHORYLATION (BY A PROLINE-DIRECTED
FT                                  KINASE) (BY SIMILARITY).
FT    MOD_RES      175    175       PHOSPHORYLATION (BY MARK) (BY
FT                                  SIMILARITY).
FT    MOD_RES      206    206       PHOSPHORYLATION (BY MARK) (BY
FT                                  SIMILARITY).
FT    MOD_RES      238    238       PHOSPHORYLATION (BY MARK) (POTENTIAL).
FT    MOD_RES      291    291       PHOSPHORYLATION (BY MARK) (BY
FT                                  SIMILARITY).
FT    MOD_RES      295    295       PHOSPHORYLATION (BY MARK) (BY
FT                                  SIMILARITY).
FT    MOD_RES      298    298       PHOSPHORYLATION (BY MARK) (BY
FT                                  SIMILARITY).
SQ    SEQUENCE   323 AA;  34131 MW;  43FDD17F CRC32;
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Query Match             30.9%;  Score 710;  DB 6;  Length 323;
Best Local Similarity   44.4%;  Pred. No. 5.9e-38;
  Matches  164;  Conservative  51;  Mismatches  78;  Indels  76;  Gaps  10;

Qy     101 TTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDG----------------TGSDDKKAK 143
           |||:     |    |::                             : |:||
Db       3 TTAAGAESAQAPSVFKQAKDKVSDG--VTKSPEKRSSLPRPSSILPPRGVSGDRDENSF 60

Qy     144 GADGKTKIATPRGAAPP----GOKGQANATRIPAKTPAPKTPPSSGEPPKSGDRSGYSS 199
           ||||   ||| :|:  :       ::|  || | |         |:|
Db      61 SLNSSISSARRTRSEPIRRAGKGGTSTPT-TPGSTAITPGTPPS-----------YSS 107

Qy     200 --PGSPGTPGSRSRTPSLPTPPP-----TREPKKVAVVRPPKSPSSAKSRLQTAPVPMPD 252
           :|     ||: |||:|  ||||      ||||:|::||   :  ||  ||:|| |
Db     108 RTPGTPGTP-SYPRPHTPGTPKSAILVPSEKVAIIRTPPKSPATPK-QLRLINQPLPD 165

Qy     253 LKNVKSKIGSTENLKHQPGGGKVQOINKKLDLSNVQSKGGSKDNIKHVPGGGSVQIVYKP 312
           ||||||||||||||||::||| |||:: |||| ||||||| ||||||||||||:|||||:
Db     166 LKNVKSKIGSTDNIKYQPKGGGQVQIVTKKIDLSH--------------------- 199
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Search completed: September 28, 2000, 20:03:00
Job time: 276 sec
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Db     166 LKNVKSKIGSTDNIKYQPKGGGQVQIVTKKIDLSH--------------------- 199
Qy     313 VDLSKVTSKCGSLGNIHHKPEGGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIE 372
           |||||||||||||||||||||||||||:||:||||||||||||||:|||:|||||||||||:
Db     200 ------VTSKCGSLKNIRHRPGGGRVKIESVKLDFKEKAQAKVGSLDNAHVPGGGNVKID 254
Qy     373 THKLTFRENAKAKTDHGAEIIVKSPVVSGDTSPRHLSNVSSTGSISIDMVDSPQLATLADEV 432
           :|:|||||||||||||||||:||    || :|| ||| : |:|
Db     255 SQKLNFREHAKARVDHGAEIITQSPGRSSVASPRLSNVSSSGSINLLESPQLATLAEDV 314
Qy     433 SASLAKQGL 441
           :|:||||||
Db     315 TAALAKQGL 323
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